SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST

Kabat

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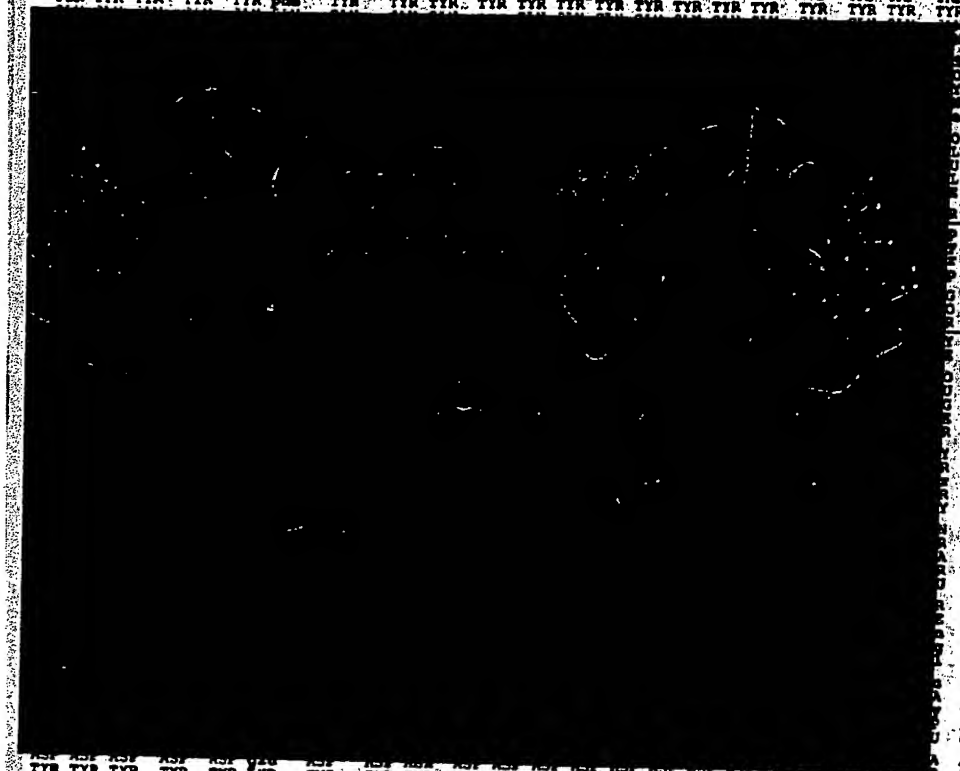

1991

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Public Health Service
National Institutes of Health

In Fig. 1 and in the stereomodels of antibody combining sites, the location of the allotypic regions may clearly be seen to be on the outside of V_H away from the combining site. Residues 9 and 65 of V_H are numbered and will facilitate location of the V_Ha allotypes. The few cDNA sequences available in 1984 (65) provided no evidence that germ line sequences encoding latent allotypes may exist in some rabbits. Since then, additional germline and expressed V_Ha sequences (63-65,188,204-206) have further refined the information on V_Ha allotypes and V_Ha^- sequences. Newer analyses of germline V_H genes of rabbits have provided examples of potential genes and pseudogenes which could generate latent allotype sequences by somatic gene conversion mechanisms (187,199,203-208). Antisera to rabbit V_Ha allotypes crossreact with human IgG, various other species of IgM and IgG, and with the Galapagos shark 7S immunoglobulin and correlate with the N-terminal amino acid sequence (209,210).

It is becoming of great importance, with all of the different mechanisms which are clearly generating diversity, to evaluate the extent to which each type of diversity, other than those resulting in pseudogenes, contributes noise rather than functional differences in complementarity of antibody combining sites (70, 211).

Ohno et al. (212,213) have proposed that the genes coding for variable domains of the light and heavy chains arose from tandem repeats of a primordial nucleotide sequence about 48 base pairs in length which subsequently diverged by mutations and deletions producing a resemblance to FR1, FR2, and FR3. The complementary strand of the primordial 48 base pair repeat of V_L became the primordial V_H. The finding (147) that the complementary strands of the human D2 and D4 minigenes coded for a portion of CDR1 of V_K tends to support this hypothesis. A 45 base pair primordial building block has also been proposed for the gene for the class I major histocompatibility complex (214).

The format of our precursor, V-region, C region sequences etc. of antibodies and T cell receptors has proven very useful in selecting primers for the polymerase chain reaction (215-217).

Constant Region Sequences

The constant region sequences were aligned in such a manner as to permit various comparisons of the light chain (C_L) and the individual domains of the heavy chain (C_H1, C_H2, C_H3, and C_H4). This was accomplished by sequential numbering on the left with gaps inserted for alignment. The following numbering system is used:

108 to 215 of C_L;
114 to 223 of C_H1, plus the first part of hinge (224 to 241), the end of hinge (242 and 243), and the first two residues of CH2 (244 and 245);
246 to 360 of C_H2;
361 to 496 of C_H3;
497 to 628 of C_H4.

The gene quadruplication in the human IgG3 hinge region (218) is numbered differently using letters 241A to 241Z, and 241AA to 241SS, and these residues should not be used in aligning domains for homology. The next two columns in the heavy chain tables indicate the EU (67) and OU (219) residue numbers, respectively. The succeeding columns which are numbered give the sequence data. The C_K and hinge domains conform to the findings of Sakano et al. (220), who defined each domain precisely by sequencing the coding and intervening nucleotide sequences bordering each domain.

The extensive nucleotide sequence data on exons for the constant regions of heavy chains have provided exact boundaries for C_H1, hinge, C_H2, C_H3, and C_H4. Usually the introns separating these domains fall within the codon for a single amino acid. We have included that amino acid residue with the domain, the exon of which contains two of the three coding nucleotides. The constant regions

HEAVY CONSTANT CHAINS CH2 REGION

EU INDEX	OU INDEX	INVARIANT RESIDUES	1 HUMAN IGM 'CL #	2 HUMAN IGM' 'CL	3 GAL	4 OU	5 BOT #	6 X17115 'CL	7 GLI #	8 HUMAN IGM MEMB 'CL	9 WAB #	10 NIG -65 #	11 ERI #	12 HUMAN IGD'CL	13 HUMAN IGD MEMB 'CL	14 HUMAN IGG3'CL #	15 OMM 'CL #	16 HER #	17 FRO #	18 JON #	19 WIS #
243A		VAL	---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
243B		PRO	---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
243C		SER	---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
243D		THR	---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
243E		PRO	---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
243F		PRO	---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
243G	230		VAL	VAL	VAL	VAL	VAL	VAL			---	---		---		---	---	---	---	---	---
243H	231		ILE	ILE	ILE	ILE	ILE	ILE			---	---		---		---	---	---	---	---	---
243I	232		ALA	ALA	ALA	ALA	ALA	ALA			---	---		---		---	---	---	---	---	---
244	231		---	---	---	---	---	---			---	---		---		ALA	ALA	ALA	ALA	ALA	ALA
245	232		---	---	---	---	---	---			---	---		---		PRO	PRO	PRO	PRO	PRO	PRO
245A			---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
245B		PRO	---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
245C			---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
246	233	233	GLU	GLU	GLX	GLU	GLU	GLU			SER	SER		SER		GLU	GLU	GLU	GLU	GLU	GLU
247	234	234	LEU	LEU	LEU	LEU	LEU	LEU			HIS	HIS		HIS		LEU	LEU	LEU	LEU	LEU	LEU
248	235	235	PRO	PRO	PRO	PRO	PRO	PRO			THR	THR		THR		LEU	LEU	LEU	LEU	LEU	LEU
249	236	236	PRO	PRO	PRO	PRO	PRO	PRO			GLN	GLN		GLN		GLY	GLY	GLY	GLY	GLY	GLY
250	237	237	LYS	LYS	LYS	LYS	LYS	LYS			PRO	PRO		PRO		GLY	GLY	GLY	GLY	GLY	GLY
251	238	238	VAL	VAL	VAL	VAL	VAL	VAL			LEU	LEU		LEU		PRO	PRO	PRO	PRO	PRO	PRO
251A		CYS	---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
251B			---	---	---	---	---	---			---	---		---		---	---	---	---	---	---
252	239	239	SER	SER	SER	SER	SER	SER			GLY	GLY		GLY		SER	SER	SER	SER	SER	SER
253	240	240	VAL	VAL	VAL	VAL	VAL	VAL			VAL	VAL		VAL		VAL	VAL	VAL	VAL	VAL	VAL
254	241	241	PHE	PHE	PHE	PHE	PHE	PHE			TYR	TYR		TYR		PHE	PHE	PHE	PHE	PHE	PHE
255	242	242	VAL	VAL	VAL	VAL	VAL	VAL			LEU	LEU		LEU		LEU	LEU	LEU	LEU	LEU	LEU
256	243		---	---	---	---	---	---			LEU	LEU		LEU		PHE	PHE	PHE	PHE	PHE	PHE
257	244	243	PRO	PRO	PRO	PRO	PRO	PRO			THR	THR		THR		PRO	PRO	PRO	PRO	PRO	PRO
258	245	244	PRO	PRO	PRO	PRO	PRO	PRO			PRO	PRO		PRO		PRO	PRO	PRO	PRO	PRO	PRO
259	246	245	ARG	ARG	ARG	ARG	ARG	ARG			ALA	ALA		ALA		LYS	LYS	LYS	LYS	LYS	LYS
260	247	246	ASP	ASP	ASP	ASX	ASP	ASP			VAL	VAL		VAL		PRO	PRO	PRO	PRO	PRO	PRO
261	248	247	GLY	GLY	GLY	GLY	GLY	GLY			GLN	GLN		GLN		LYS	LYS	LYS	LYS	LYS	LYS
262	249	248	PHE	PHE	PHE	PHE	PHE	PHE			ASP	ASP		ASP		ASP	ASP	ASP	ASP	ASP	ASP
263	250		---	---	---	---	---	PHE			---	---		---		THR	THR	THR	THR	THR	THR
264	251	249	PHE	PHE	PHE	PHE	PHE	GLY			LEU	LEU		LEU		LEU	LEU	LEU	LEU	LEU	LEU
265	252	250	GLY	GLY	GLY	GLY	GLY	ASN			TRP	TRP		TRP		MET	MET	MET	MET	MET	MET
266	253	251	ASN	ASN	ASX	ASX	ASN	PRO			LEU	LEU		LEU		ILE	ILE	ILE	ILE	ILE	ILE
267	254	252	PRO	PRO	PRO	PRO	PRO	ARG			ARG	ARG		ARG		SER	SER	SER	SER	SER	SER
268	255	253	ARG	ARG	ARG	ARG	ARG	SER			ASP	ASP		ASP		ARG	ARG				ARG
269	256	254	LYS	LYS	LYS	LYS	LYS	LYS			LYS	LYS		LYS		THR	THR				THR
270	257	255	SER	SER	SER	SER	SER	SER			ALA	ALA		ALA		PRO	PRO				PRO
271	258	256	LYS	LYS	LYS	LYS	LYS	LYS			THR	THR		THR		GLU	GLU				GLU
272	259	257	LEU	LEU	LEU	LEU	LEU	LEU			PHE	PHE		PHE		VAL	VAL				VAL
273	260	258	ILE	ILE	ILE	ILE	ILE	ILE			THR	THR		THR		THR	THR				THR
274	261	259	CYS	CYS	CYS	CYS	CYS	CYS			CYS	CYS		CYS		CYS	CYS				CYS
275	262	260	GLN	GLN	GLN	GLN	GLN	GLN			PHE	PHE		PHE		VAL	VAL				VAL
276	263	261	ALA	ALA	ALA	ALA	ALA	ALA			VAL	VAL		VAL		VAL	VAL				VAL
277	264	262	THR	THR	THR	THR	THR	THR			VAL	VAL		VAL		VAL	VAL				VAL
278	265	263	GLY	GLY	GLY	GLY	GLY	GLY			GLY	GLY		GLY		ASP	ASP				ASP
279	266	264	PHE	PHE	PHE	PHE	PHE	PHE			SER	SER		SER		VAL	VAL				VAL
280	267	265	SER	SER	SER	SER	SER	SER			ASP	ASP		ASP		SER	SER				SER
281	268	266	PRO	PRO	PRO	PRO	PRO	PRO			LEU	LEU		LEU		HIS	HIS				HIS
282	269	267	ARG	ARG	ARG	ARG	ARG	ARG			LYS	LYS		LYS		GLU	GLU				GLU
283	270	268	GLN	GLN	GLN	GLN	GLN	GLN			ASP	ASP		ASP		ASP	ASP				ASP
284	271		ILE	ILE	ILE	---	ILE	ILE			---	---		---		PRO	PRO				PRO
285	272		GLN	GLN	GLN	---	GLU	GLN			ALA	ALA		ALA		GLU					GLU
286	273	269	VAL	VAL	VAL	VAL	VAL	VAL			---	---		---		VAL	VAL				VAL
287	274		---	---	---	---	---	---			HIS	HIS		HIS		GLN	GLN				GLN
288	275		---	---	---	---	---	---			LEU	LEU		LEU		PHE	PHE				PHE
289	276	270	SER	SER	SER	TRP	SER	SER			THR	THR		THR		LYS	LYS				LYS
290	277	271	TRP	TRP	TRP	SER	TRP	TRP			TRP	TRP		TRP		TRP	TRP				TRP
291	278	272	LEU	LEU	LEU	LEU	LEU	LEU			GLU	GLU		GLU		TYR	TYR				TYR
292	279	273	ARG	ARG	ARG	ARG	ARG	ARG			VAL	VAL		VAL		VAL	VAL				VAL
293		274	GLU	GLU	GLU	GLU	GLU	GLU			---	---		---		---	---				---
294		275	GLY(.95)	GLY	GLY	GLY	GLY	GLY	GLY		---	---		---		---	---				---
295	280	276	LYS	LYS	LYS	LYS	LYS	LYS			ALA	ALA		ALA		ASP	ASP				ASP
296	281	277	GLN	GLN	GLN	GLN	GLN	GLN			GLY	GLY		GLY		GLY	GLY				GLY
297		278	VAL	VAL	VAL	VAL	VAL	VAL			LYS	LYS		LYS		---	---				---
298		279	GLY	GLY	GLY	GLY	GLY	GLY			---	---		---		---	---				---
299	282	280	SER	SER	SER	SER	SER	SER			VAL	VAL		VAL		VAL	VAL				VAL
300	283	281	GLY	GLY	GLY	GLY	GLY	GLY			PRO	PRO		PRO		GLU	GLU				GLN
301	284	282	VAL	VAL	VAL	VAL	VAL	VAL			THR	THR		THR		VAL	VAL				VAL
302	285	283	THR	THR	THR	THR	THR	THR			GLY	GLY		GLY		HIS	HIS				HIS
303	286		---	---	---	---	---	---			GLY	GLY		GLY		ASN	ASN				ASN
304	287	284	THR	THR	THR	THR	THR	THR			VAL	VAL		VAL		ALA	ALA				ALA
305	288	285	ASP	ASP	ASN	ASX	ASP	ASP			GLU	GLU		GLU		LYS	LYS				LYS
306	289	286	GLN	GLN	GLU	GLX	GLU	GLN			GLU	GLU		GLU		THR	THR				THR
307	290	287	VAL	VAL	VAL	VAL	VAL	VAL			GLY	GLY		GLY		LYS	LYS				LYS
308	291	288	GLN	GLN	GLX	GLX	GLU	GLN			LEU	LEU		LEU		PRO	LEU				PRO
309	292	289	ALA	ALA	ALA	ALA	ALA	ALA			LEU	LEU		LEU		ARG	ARG				ARG
310	293	290	GLU	GLU	GLX	GLX	GLU	GLU			GLU	GLU		GLU		GLU	GLU				GLU
311	294	291	ALA	ALA	ALA	ALA	ALA	ALA			ARG	ARG		ARG		GLU	GLU				GLN
312	295	292	LYS	LYS	LYS	LYS	LYS	LYS			HIS	HIS		HIS		GLN	GLN				GLN
313	296	293	GLU	GLU	GLU	GLX	GLU	GLU			SER	SER		SER		TYR	TYR				PHE
314	297	294	SER	SER	SER	SER	SER	SER			ASN	ASN		ASN		ASN	ASN				ASN
315		295	GLY	GLY	GLY	GLY	GLY	GLY			---	---		---		---	---				---
316		296	PRO	PRO	PRO	PRO	PRO	PRO			---	---		---		---	---				---
317	298	297	THR	THR	THR	THR	THR	THR			GLY	GLY		GLY		---	---				---
318	299	298	THR	THR	THR	THR	THR	THR			SER	SER		SER		SER	SER				SER
319	300	299	TYR	TYR	TYR	TYR	TYR	TYR			GLN	GLN		GLN		PHE	PHE				PHE
320	301	300	LYS	LYS	LYS	LYS	LYS	LYS			SER	SER		SER		ARG	ARG				ARG
321	302	301	VAL	VAL	VAL	VAL	VAL	VAL			GLN	GLN		GLN		VAL	VAL				VAL
322	303	302	THR	THR	THR	THR	THR	THR			HIS	HIS		HIS		VAL	VAL				VAL
323	304	303	SER(.95)	SER	SER	SER	SER	SER			SER	SER		SER		SER	SER				SER
324	305	304	THR	THR	THR	THR	THR	THR			ARG	ARG		ARG		VAL	VAL				VAL
325	306	305	LEU	LEU	LEU	LEU	LEU	LEU			LEU	LEU		LEU		LEU	LEU				LEU
326	307	306	THR	THR	THR	THR	THR	THR			THR	THR		THR		THR	THR				THR
327	308	307	ILE	ILE	ILE	ILE	ILE	ILE			LEU	LEU		LEU		VAL	VAL				VAL
328	309	308	LYS	LYS	LYS	LYS	LYS	LYS			PRO	PRO		PRO		LEU	LEU				LEU
329	310	309	GLU	GLU	GLU	GLX	GLU	GLU			ARG	ARG		ARG		HIS	HIS				HIS
330	311	310		SER	SER	SER	SER	SER			SER	SER		SER		GLN	GLN				GLN
331	312	311		ASP	ASX	ASP	ASP	ASP			LEU	LEU		LEU		ASP	ASP				ASN
332	313	312	TRP(.95)	TRP	TRP	TRP	TRP	TRP			TRP	TRP		TRP		TRP	TRP				TRP
333	314	313		LEU	LEU	LEU	LEU	LEU			ASN	ASN		ASN		LEU	LEU				LEU
				---	---	---	---	---			---	---		---		---	---				---
				---	---	---	---	---			---	---		---		---	---				---
334	315	314		GLY	SER	GLY	GLY	SER			ALA	ALA		ALA		ASN	ASN				---
335	316	315		GLN	GLN	GLU	GLN	GLN			GLY	GLY		GLY		GLY	GLY				ASP
336	317	316		SER	SER	SER	SER	SER			THR	THR		THR		LYS	LYS				GLY
337	318	317		MET	MET	MET	MET	MET			SER	SER		SER		GLU	GLU				LYS
338	319	318		PHE	PHE	PHE	PHE	PHE			VAL	VAL		VAL		TYR	TYR				GLU
339	320	319		THR	THR	THR	THR	THR			THR	THR		THR		LYS	LYS				TYR
340	321	320	CYS(.98)	CYS	CYS	CYS	CYS	CYS			CYS	CYS		CYS		CYS	CYS				LYS
341	322	321		ARG	ARG	ARG	ARG	ARG			THR	THR		THR		LYS	LYS				CYS
342	323	322		VAL	VAL	VAL	VAL	VAL			LEU	LEU		LEU		VAL	VAL				LYS
343	324	323	ASP	ASP	ASP	ASP	ASP	ASP			ASN	ASN		ASN		SER	SER				VAL
344	325	324	HIS	HIS	HIS	HIS	HIS	HIS			HIS	HIS		HIS		ASN	ASN				SER
345	326	325	ARG	ARG	ARG	ARG	ARG	ARG			PRO	PRO		PRO		LYS	LYS				ASN
346	327	326	GLY	GLY	GLY	GLY	GLY	GLY			SER	SER		SER		ALA	ALA				LYS
347	328	327	LEU	LEU	LEU	LEU	LEU	LEU			LEU	LEU		LEU		LEU	LEU				ALA
348	329	328	THR	THR	THR	THR	THR	THR			PRO	PRO		PRO		PRO	PRO				LEU
349	330	329	PHE	PHE	PHE	PHE	PHE	PHE			PRO	PRO		PRO		ALA	ALA				PRO
350	331	330	GLN	GLN	GLN	GLN	GLN	GLN			GLN	GLN		GLN		PRO	PRO				ALA
351	332	331	GLN	GLN	GLN	GLN	GLN	GLN			ARG	ARG		ARG		ILE	ILE				PRO
351A			---	---	---	---	---	---			---	---		---		---	---				ILE
352	333	332	ASN	ASN	ASX	ASN	ASN	ASN			LEU	LEU		LEU		GLU	GLU				---
353	334	333	ALA	ALA	ALA	ALA	ALA	ALA			MET	MET		MET		LYS	LYS				GLU
354	335	334	SER	SER	SER	SER	SER	SER			ALA	ALA		ALA		THR	THR				LYS
355	336	335	SER	SER	SER	SER	SER	SER			LEU	LEU		LEU		ILE	ILE				THR
356		336	MET	MET	MET	MET	MET	MET			---	---		---		---	---				ILE
357	337	337	CYS	CYS	CYS	CYS	CYS	CYS			---	---		---		---	---				---
358	338	338	VAL	VAL	VAL	VAL	GLY	VAL			ARG	ARG		ARG		SER	SER				SER
359	339	339	PRO	PRO	PRO	PRO	PRO	PRO			GLU	GLU		GLU		LYS	LYS				LYS
360	340		---	---	---	---	---	---			PRO	PRO		PRO		THR	ALA				THR
											ALA	ALA		ALA		LYS	LYS				LYS

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

EU INDEX	OU INDEX	20 SPA	21 ZUC	22 ZUC'	23 KUP	24 BRU	25 JIR	26 CHA	27 GOE	28 EU	29 NIE	30 CRA	31 VAU	32 LEB	33 EST	34 YOK	35 SAC	36 HUMAN IGG1 γ-CH	37 KOL	38 MCG	39 LEC	40 DOB	41 BUR	42 TRO	43 CAR
243A			---	---	---	---		---		---	---				---	---		---	---	---	---	---	VAL	VAL	
243B			---	---	---	---		---		---	---				---	---		---	---	---	---	---	PRO	PRO	
243C			---	---	---	---		---		---	---				---	---		---	---	---	---	---	SER	SER	
243D			---	---	---	---		---		---	---				---	---		---	---	---	---	---	THR	THR	THR
243E			---	---	---	---		---		---	---				---	---		---	---	---	---	---	PRO	PRO	PRO
243F			---	---	---	---		---		---	---				---	---		---	---	---	---	---			
243G		230	---	---	---	---		---		---	---				---	---		---	---	---	---	---	PRO	PRO	PRO
243H		231	---	---	---	---		---		---	---				---	---		---	---	---	---	---	THR	THR	THR
243I		232	---	---	---	---		---		---	---				---	---		---	---	---	---	---	PRO	PRO	PRO
244	231		ALA	ALA	ALA	ALA		ALA		ALA	ALA				---	---		---	---	---	---	---	SER	SER	SER
245	232		PRO	PRO	PRO	PRO		PRO		PRO	PRO				ALA	ALA		ALA	ALA	ALA	ALA	ALA	PRO	PRO	PRO
245A			---	---	---	---		---		---	---				---	---		PRO	PRO	PRO	PRO	PRO	SER	SER	SER
245B			---	---	---	---		---		---	---				---	---		---	---	---	---	---	THR	THR	THR
245C			---	---	---	---		---		---	---				---	---		---	---	---	---	---	PRO	PRO	PRO
246	233	233	GLU	GLU	GLU	GLU		GLU		GLU	GLN				---	---		GLU	GLU	GLU	GLX	GLU	PRO	PRO	PRO
247	234	234	LEU	LEU	LEU	LEU		LEU		LEU	LEU				---	---		LEU	LEU	LEU	LEU	LEU	THR	THR	THR
248	235	235	LEU	LEU				LEU		LEU	LEU				---	---		LEU	LEU	LEU		LEU	PRO	PRO	PRO
249	236	236	GLY	GLY				GLY		GLY	GLY				---	---		LEU	LEU	LEU		LEU	SER	SER	SER
250	237	237	GLY	GLY				GLY		GLY	GLY				---	---		GLY	GLY	GLY		GLY	PRO	PRO	PRO
251	238	238	PRO	PRO				PRO		PRO	PRO				---	---		GLY	GLY	GLY		GLY	SER	SER	SER
251A			---	---				---		---	---				---	---		PRO	PRO	PRO		PRO	CYS	CYS	CYS
251B			---	---				---		---	---				---	---		---	---	---		---	CYS	CYS	CYS
252	239	239	SER	SER				SER		SER	SER				---	---		---	---	---		---	HIS	HIS	HIS
253	240	240	VAL	VAL				VAL		VAL	VAL				---	---		SER	SER	SER		SER	PRO	PRO	PRO
254	241	241	PHE	PHE				PHE		PHE	PHE				---	---		VAL	VAL	VAL		VAL	ARG	ARG	ARG
255	242	242	LEU	LEU				LEU		LEU	LEU				---	---		PHE	PHE	PHE			LEU	LEU	LEU
256	243		PHE	PHE				PHE		PHE	PHE				---	---		LEU	LEU	LEU			SER	SER	
257	244	243	PRO	PRO				PRO		PRO	PRO				---	---		PHE	PHE	PHE			LEU	LEU	
258	245	244	PRO	PRO				PRO		PRO	PRO				---	---		PRO	PRO	PRO			HIS	HIS	
259	246	245	LYS	LYS				LYS		LYS	LYS				---	---		PRO	PRO	PRO			ARG	ARG	
260	247	246	PRO	PRO				PRO		PRO	PRO				---	---		LYS	LYS	LYS			PRO	PRO	
261	248	247	LYS	LYS				LYS		LYS	LYS				---	---		PRO	PRO	PRO			ALA	ALA	
262	249	248	ASP					ASP		ASP	ASP				---	---		LYS	LYS	LYS			LEU	LEU	
263	250		THR					---		THR	THR				---	---		ASP	ASP	ASP			GLN	GLN	
264	251	249	LEU					LEU		LEU	LEU				---	---		THR	THR	THR			ASP	ASN	
265	252	250	MET					MET	MET	MET	MET				---	---		LEU	LEU	LEU			LEU	LEU	
266	253	251	ILE				ILE	ILE	ILE	ILE	ILE				---	---		MET	MET	MET			LEU	LEU	
267	254	252	SER				SER		SER	SER	SER				---	---		ILE	ILE	ILE			LEU	LEU	
268	255	253	ARG				ARG		ARG	ARG	ARG				---	---		SER	SER	SER			GLY	GLY	
269	256	254	THR				THR		THR	THR	THR				---	---		ARG	ARG	ARG			SER	SER	
270	257	255	PRO				PRO		PRO	PRO	PRO				---	---		THR	THR	THR			GLU	GLN	
271	258	256	GLU				GLU		GLU	GLU	GLU				---	---		PRO	PRO	PRO			ALA	ALA	
272	259	257	VAL				VAL		VAL	VAL	VAL				---	---		GLU	GLU	GLX			ASN	ASN	
273	260	258	THR				THR		THR	THR	THR				---	---		VAL	VAL	VAL			LEU	LEU	
274	261	259	CYS				CYS		CYS	CYS	CYS				---	---		THR	THR	THR			THR	THR	
275	262	260	VAL				VAL		VAL	VAL	VAL				---	---		CYS	CYS				CYS	CYS	
276	263	261	VAL				VAL		VAL	VAL	VAL				---	---		VAL	VAL	VAL			THR	THR	
277	264	262	VAL				VAL		VAL	VAL	VAL				---	---		VAL	VAL	VAL			LEU	LEU	
278	265	263	ASP				ASP		ASP	ASP	ASP				---	---		VAL	VAL	VAL			THR	THR	
279	266	264	VAL				VAL		VAL	VAL	VAL				---	---		ASP	ASP				GLY	GLY	
280	267	265	SER				SER		SER	SER	SER				---	---		VAL	VAL				LEU	LEU	
281	268	266	HIS				HIS		HIS	HIS	HIS				---	---		SER	SER				ARG	ARG	
282	269	267	GLU				GLU		GLU	GLU	GLU				---	---		HIS	HIS				ASP	ASP	
283	270	268	ASP				ASP		ASP	ASP	ASP				---	---		GLU	GLU				ALA	ALA	
284	271		PRO				PRO		PRO	PRO	PRO				---	---		ASP	ASP				SER	SER	
285	272		GLX				GLU		GLU	GLN	GLU				---	---		PRO	PRO				---	---	
286	273	269	VAL				VAL		VAL	VAL	VAL				---	---		GLU	GLU				GLY	GLY	
287	274		GLX				GLN		GLN	LYS	LYS				---	---		VAL	VAL				VAL	VAL	
288	275		PHE				PHE		PHE	PHE	PHE				---	---		LYS	LYS				THR	THR	
289	276	270	LYS				LYS		LYS	ASN	ASN				---	---		PHE	PHE				PHE	PHE	
290	277	271					TRP		TRP	TRP	TRP				---	---		ASN	ASN				THR	THR	
291	278	272					TYR		TYR	TYR	TYR				---	---		TRP	TRP				TRP	TRP	
292	279	273	TYR				VAL		VAL	VAL	VAL				---	---		TYR	TYR				PRO	THR	
293		274	VAL				---		---	---	---				---	---		VAL	VAL				SER	PRO	
294		275	---				---		---	---	---				---	---		---	---				---	---	
295	280	276	ASP				ASP		ASP	ASP	ASP				---	---		---	---				---	---	
296	281	277	GLY				GLY		GLY	GLY	GLY				---	---		ASP	ASP				THR	SER	
297		278	---				---		---	---	---				---	---		GLY	GLY				SER	SER	
298		279	---				---		---	---	---				---	---		---	---				---	---	
299	282	280	VAL				VAL		VAL	VAL	VAL				---	---		---	---				---	---	
300	283	281					GLN		GLN	GLN	GLU				---	---		VAL	VAL				GLY	GLY	
301	284	282					VAL		VAL	VAL	VAL				---	---		GLU	GLU				LYS	LYS	
302	285	283					HIS		HIS	HIS	HIS				---	---		VAL	VAL				SER	SER	
303	286						ASN		ASN	ASN	ASN				---	---		HIS	HIS				ALA	ALA	
304	287	284	ASN ALA				ALA		ALA	ALA	ALA				---	---		ASN	ASN				VAL	VAL	
305	288	285	LYS				LYS		LYS	LYS	LYS				---	---		ALA	ALA				GLN	GLN	
306	289	286	THR				THR		THR	THR	THR				---	---		LYS	LYS				GLY	GLY	
307	290	287	LYS				LYS		LYS	LYS	LYS				---	---		THR	THR				PRO	PRO	
308	291	288	PRO				PRO		PRO	PRO	PRO				---	---		LYS	LYS				PRO	PRO	
309	292	289	ARG				ARG		ARG	ARG	ARG				---	---		PRO	PRO				GLU	ASP	
310	293	290	GLX				GLU		GLU	GLU					---	---		ARG	ARG				ARG	ARG	
311	294	291	GLX				GLN		GLN	GLU					---	---		GLU	GLU				ASP	ASP	
312	295	292	GLX				GLN		GLN	GLN					---	---		GLN	GLN				LEU	LEU	
313	296	293	PHE				TYR		TYR	TYR					---	---		TYR	TYR				CYS	CYS	
314	297	294	ASX				ASN		ASX	ASX					---	---		---	---				GLY	GLY	
315		295	---				---		---	---					---	---		ASN	ASN				CYS	CYS	
316		296	---				---		---	---					---	---		---	---				---	---	
317	298	297	SER				SER		SER	SER					---	---		---	---				---	---	
318	299	298	THR				THR		THR	THR					---	---		SER	SER				---	---	
319	300	299	PHE				PHE		TYR	TYR					---	---		THR	THR				---	---	
320	301	300	ARG				ARG		ARG	ARG					---	---		TYR	TYR				TYR	TYR	
321	302	301	VAL				VAL		VAL	VAL					---	---		ARG	ARG				SER	SER	
322	303	302	VAL				VAL		VAL	VAL					---	---		VAL	VAL				VAL	VAL	
323	304	303	SER				SER		SER	SER					---	---		VAL	VAL				SER	SER	
324	305	304	VAL				VAL		VAL	VAL					---	---		SER	SER				SER	SER	
325	306	305	LEU				LEU		LEU	LEU					---	---		VAL	VAL				VAL	VAL	
326	307	306	THR				THR		THR	THR					---	---		LEU	LEU				LEU	LEU	
327	308	307	VAL				VAL	THR	THR	THR					---	---		THR	THR				PRO	SER	
328	309	308	LEU				LEU		VAL	VAL					---	---		VAL	VAL				GLY	GLY	
329	310	309	HIS				HIS		LEU	LEU					---	---		LEU	LEU				CYS	CYS	
330	311	310	GLX				GLN		HIS	HIS					---	---		HIS	HIS				ALA	ALA	
331	312	311					ASN		GLN	GLN					---	---		GLN	GLN				GLU	GLN	
332	313	312					TRP		ASN	ASP					---	---		ASP	ASP				PRO	PRO	
333	314	313					LEU		TRP	TRP					---	---		TRP	TRP				TRP	TRP	
334	315	314					ASP		LEU	LEU					---	---		LEU	LEU				ASN	ASP	
335	316	315					GLY		ASX	ASP					---	---		---	---				---	---	
336	317	316	LYS				LYS		GLY	GLY					---	---		ASN	ASP				HIS	HIS	
337	318	317	GLU				GLU		LYS	LYS					---	---		GLY	GLY				GLY	GLY	
338	319	318	TYR				TYR		GLU	GLU					---	---		LYS	LYS				LYS	LYS	
339	320	319	LYS				LYS		TYR	TYR					---	---		GLU	GLU				THR	THR	
340	321	320	CYS				CYS		LYS	LYS					---	---		TYR	TYR				PHE	PHE	
341	322	321	LYS				LYS		CYS	CYS					---	---		LYS	LYS				THR	THR	
342	323	322	VAL				VAL		LYS	LYS					---	---		CYS	CYS				CYS	CYS	
343	324	323	SER				SER		VAL	VAL					---	---		LYS	LYS				THR	THR	
344	325	324	ASN				ASN		SER	SER					---	---		VAL	VAL				ALA	ALA	
345	326	325	LYS				LYS		ASN	ASN					---	---		SER	SER				ALA	ALA	
346	327	326	ALA				ALA		LYS	LYS					---	---		ASN	ASN				TYR	TYR	
347	328	327	LEU				LEU		ALA	ALA					---	---		LYS	LYS				PRO	PRO	
348	329	328	PRO				PRO		LEU	LEU					---	---		ALA	ALA				GLU	GLU	
349	330	329	ALA				ALA		PRO	PRO					---	---		LEU	LEU				SER	SER	
350	331	330	PRO				PRO		ALA	ALA					---	---		PRO	PRO				LYS	LYS	
351	332	331	ILE				ILE		PRO	PRO					---	---		ALA	ALA				THR	THR	
351A			---				---		ILE	ILE					---	---		PRO	PRO				PRO	PRO	
352	333	332	GLU				GLU		---	---					---	---		ILE	ILE				LEU	LEU	
353	334	333	LYS				LYS		GLU	GLU					---	---		---	---				---	---	
354	335	334	THR				THR		LYS	LYS					---	---		GLU	GLU				THR	THR	
355	336	335	ILE				ILE		THR	THR					---	---		LYS	LYS				ALA	ALA	
356		336	---				---		ILE	ILE					---	---		THR	THR				THR	THR	
357	337	337	SER				SER		---	---					---	---		ILE	ILE				LEU	LEU	
358	338	338	LYS				LYS		SER	SER					---	---		---	---				---	---	
359	339	339	THR				THR		LYS	LYS					---	---		SER	SER				SER	SER	
360	340		LYS				LYS		ALA	ALA					---	---		LYS	LYS				LYS	LYS	
									LYS	LYS								ALA	ALA				---	---	
																		LYS	LYS				SER	SER	

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

	EU INDEX	OU INDEX	44 CHIMPANZEE CH4-14 (IGG1) 'CL	45 HUMAN IGA1 'CL	46 GORILLA IGA1'CL	47 HUMAN IGG'CL ϕ	48 HUMAN IGG2 'CL ϕ	49 TIL	50 ZIE	51 SA	52 PIG	53 HUMAN IGG4 'CL ϕ	54 VIN	55 HUMAN IGE'CL ϕ	56 HUMAN IGE 'CL' ϕ	57 CHIMP IGE 'CL	58 ORANGUTAN IGE'CL	59 U266 'CL	60 ND	61 BUT	62 LAN
243A			---	VAL	VAL	---	---	---		---		---	---	---	---	---	---	---	---	---	---
243B			---	PRO	PRO	---	---	---		---		---	---	---	---	---	---	---	---	---	---
243C			---	SER	SER	---	---	---		---		---	---	---	---	---	---	---	---	---	---
243D			---	THR	THR	---	---	---		---		---	---	---	---	---	---	---	---	---	---
243E			---	PRO	PRO	---	---	---		---		---	---	---	---	---	---	---	---	---	---
243F			---	PRO	PRO	---	---	---		---		---	---	---	---	---	---	---	---	---	---
243G		230	---	THR	THR	---	---	---		---		---	---	VAL	---	VAL	VAL	VAL	VAL	---	---
243H		231	---	PRO	PRO	---	---	---		---		---	---	CYS	---	CYS	CYS	CYS	CYS	---	---
243I		232	---	SER	SER	---	---	---		---		---	---	SER	---	SER	SER	SER	SER	---	---
244	231		ALA	PRO	PRO	THR	ALA	ALA		ALA		ALA	ALA	---	---	---	---	---	---	---	---
245	232		PRO	SER	SER	THR	PRO	PRO				PRO		---	---	---	---	---	---	---	---
245A			---	THR	THR	---	---	---				---	---	---	---	---	---	---	---	---	---
245B			---	PRO	PRO	---	---	---				---	---	---	---	---	---	---	---	---	---
245C			---	PRO	PRO	---	---	---				---	---	---	---	---	---	---	---	VAL	VAL
246	233	233	GLU	THR	THR	GLU	PRO	PRO				GLU		ARG	---	ARG	ARG	ARG	ARG	PRO	PRO
247	234	234	LEU	PRO	PRO	PRO	VAL	VAL				PHE	PHE	ASP	---	ASP	ASP	ASP	ASX	PRO	PRO
248	235	235	LEU	SER	SER	LEU	ALA	ALA				LEU	LEU	PHE	PHE	PHE	PHE	PHE	PHE	PRO	PRO
249	236	236	GLY	PRO	PRO	GLY	---	---				GLY	GLY	THR	THR	THR	THR	THR	THR	PRO	PRO
250	237	237	GLY	SER	PRO	GLY	GLY	GLY				GLY	GLY	PRO	PRO	---	PRO	PRO	PRO	PRO	PRO
251	238	238	PRO	CYS	CYS	PRO	PRO	PRO				PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	CYS	CYS
251A			---	CYS	CYS	---	---	---				---	---	---	---	---	---	---	---	CYS	CYS
251B			---	HIS	HIS	---	---	---				---	---	---	---	---	---	---	---	HIS	HIS
252	239	239	SER	PRO	PRO	SER	SER	SER				SER	SER	THR	THR	THR	THR	THR	THR	PRO	PRO
253	240	240	VAL	ARG	ARG	VAL	VAL	VAL				VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ARG	ARG
254	241	241	PHE	LEU	LEU	PHE	PHE	PHE				PHE	PHE	LYS	LYS	LYS	LYS	LYS	LYS	LEU	LEU
255	242	242	LEU	SER	SER	LEU	LEU	LEU				LEU	LEU	ILE	ILE	VAL	ILE	ILE	ILE	SER	SER
256	243		PHE	LEU	LEU	PHE	PHE	PHE				PHE	PHE	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
257	244	243	PRO	HIS	HIS	PRO	PRO	PRO				PRO	PRO	GLN	GLN	GLN	GLN	GLN	GLX	HIS	HIS
258	245	244	PRO	ARG	ARG	PRO	PRO	PRO				PRO	PRO	SER	SER	SER	SER	SER	SER	ARG	ARG
259	246	245	LYS	PRO	PRO	LYS	LYS	LYS				LYS	LYS	SER	SER	SER	SER	SER	SER	PRO	PRO
260	247	246	PRO	ALA	ALA	PRO	PRO	PRO				PRO	PRO	CYS	CYS	CYS	CYS	CYS	CYS	ALA	ALA
261	248	247	LYS	LEU	LEU	LYS	LYS	LYS				LYS	LYS	ASP	ASP	ASP	ASP	ASP	ASX	LEU	LEU
262	249	248	ASP	GLU	GLU	ASP	ASP	ASP				ASP	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLU	GLU
263	250		THR	ASP	ASP	THR	THR	THR				THR	THR	GLY	GLY	GLY	GLY	GLY	LEU	ASP	ASP
264	251	249	LEU	LEU	LEU	LEU	LEU	LEU				LEU	LEU	GLY	GLY	GLY	GLY	GLY	GLY	LEU	LEU
265	252	250	MET	LEU	LEU	MET	MET	MET				MET	MET	HIS	HIS	HIS	HIS	HIS	HIS	LEU	LEU
266	253	251	ILE	LEU	LEU	ILE	ILE	ILE	ILE			ILE	ILE	PHE	PHE	PHE	PHE	PHE	PHE	LEU	LEU
267	254	252	SER	GLY	GLY	SER	SER	SER	SER			SER	SER	PRO	PRO	PRO	PRO	PRO	GLY	GLY	GLY
268	255	253	ARG	SER	SER	ARG	ARG	ARG	ARG			ARG	ARG	PRO	PRO	PRO	LEU	PRO	PRO	SER	SER
269	256	254	THR	GLU	GLU	THR	THR	THR	THR			THR	THR	THR	THR	THR	THR	THR	THR	GLU	GLU
270	257	255	PRO	ALA	ALA	PRO	PRO	PRO	PRO			PRO	PRO	ILE	ILE	ILE	ILE	ILE	ILE	ALA	ALA
271	258	256	GLU	ASN	ASN	GLU	GLU	GLU	GLU			GLU	GLU	GLN	GLN	GLN	GLN	GLN	GLX	ASN	ASN
272	259	257	VAL	LEU	LEU	VAL	VAL	VAL	VAL			VAL	VAL	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
273	260	258	THR	THR	THR	THR	THR	THR	THR			THR	THR	LEU	LEU	LEU	LEU	LEU	---	THR	THR
274	261	259	CYS	CYS	CYS	CYS	CYS	CYS	CYS			CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
275	262	260	VAL	THR	THR	VAL	VAL	VAL	VAL			VAL	VAL	LEU	LEU	LEU	LEU	LEU	LEU	THR	THR
276	263	261	VAL	LEU	LEU	VAL	VAL	VAL	VAL			VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LEU	LEU
277	264	262	VAL	THR	THR	VAL	VAL	VAL	VAL			VAL	VAL	SER	SER	SER	SER	SER	SER	THR	THR
278	265	263	ASP	GLY	GLY	ASP	ASP	ASP	ASP			ASP	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
279	266	264	VAL	LEU	LEU	VAL	VAL	VAL	VAL			VAL	VAL	TYR	TYR	TYR	TYR	TYR	TYR	LEU	LEU
280	267	265	SER	ARG	ARG	SER	SER	SER	SER			SER	SER	THR	THR	THR	THR	THR	THR	ARG	ARG
281	268	266	HIS	ASP	ASP	HIS	HIS	HIS	HIS			GLN	GLN	---	---	---	---	---	---	ASP	ASP
282	269	267	GLU	ALA	ALA	GLU	GLU	GLU	GLU			GLU	GLU	---	---	---	---	---	---	ALA	ALA
283	270	268	ASP	SER	SER	ASP	ASP	ASP	ASP			ASP	ASP	---	---	---	---	---	---	SER	SER
284	271		PRO	---	---	PRO	PRO	PRO	PRO			PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	---	---
285	272		GLU	GLY	GLY	GLU	GLU	GLU	GLU			GLU	GLX	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
286	273	269	VAL	VAL	VAL	VAL	VAL	VAL	VAL			VAL		THR	THR	THR	THR	THR	THR	ALA	ALA
287	274		LYS	THR	THR	LYS	GLN	GLN	GLN			GLN		ILE	ILE	ILE	ILE	ILE	ILE	THR	THR
288	275		PHE	PHE	PHE	PHE	PHE	PHE	PHE			PHE		ASN	ASN	ASN	ASN	ASN	ASN	PHE	PHE
289	276	270	ASN	THR	THR	ASN	ASN	ASN	ASN			ASN	ASN	ILE	ILE	ILE	ILE	ILE	ILE	THR	THR
290	277	271	TRP	TRP	TRP	TRP	TRP	TRP	TRP			TRP	TRP	THR	THR	THR	THR	THR	THR	TRP	TRP
291	278	272	TYR	THR	THR	TYR	TYR	TYR	TYR			TYR	TYR	TRP	TRP	TRP	TRP	TRP	PRO	PRO	PRO
292	279	273	VAL	PRO	PRO	VAL	VAL	VAL	VAL			VAL	VAL	LEU	LEU	LEU	LEU	LEU	LEU	SER	SER
293		274	---	---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---
294		275	---	---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---
295	280	276	ASP	SER	SER	ASP	ASP	ASP	ASP			ASP	ASP	GLU	GLU	GLU	GLU	GLU	GLX	---	---
296	281	277	GLY	SER	SER	GLY	GLY	GLY	GLY			GLY	GLY	ASP	ASP	ASP	ASP	ASP	ASX	SER	SER
297		278	---	---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---
298		279	---	---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---
299	282	280	VAL	GLY	GLY	VAL	VAL	VAL	VAL			VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
300	283	281	GLU	LYS	LYS	GLU	GLU	GLU	GLU			GLU	GLU	GLN	GLN	GLN	GLN	GLN	GLX	LYS	LYS
301	284	282	VAL	SER	SER	VAL	VAL	VAL	VAL			VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	SER	SER
302	285	283	HIS	ALA	ALA	HIS	HIS	HIS	HIS			HIS	HIS	MET	MET	MET	MET	MET	MET	ALA	ALA
303	286		ASN	VAL	VAL	ASN	ASN	ASN	ASN			ASN	ASN	---	---	---	---	---	---	VAL	VAL
304	287	284	ALA	GLN	GLU	ALA	ALA	ALA	ALA			ALA	ALA	ASP	ASP	ASP	ASP	ASP	ASP	GLU	GLU
305	288	285	LYS	GLY	GLY	LYS	LYS	LYS	LYS			LYS	LYS	VAL	VAL	VAL	VAL	VAL	VAL	GLY	GLY
306	289	286	THR	PRO	PRO	THR	THR	THR	THR			THR	THR	ASP	ASP	ASP	ASP	ASP	ASP	PRO	PRO
307	290	287	LYS	PRO	PRO	LYS	LYS	LYS	LYS			LYS	LYS	LEU	LEU	LEU	LEU	LEU	LEU	PRO	PRO
308	291	288	PRO	GLU	GLU	PRO	PRO	PRO	PRO			PRO	PRO	SER	SER	SER	SER	SER	SER	GLU	GLU
309	292	289	ARG	ARG	ARG	TRP	ARG	ARG	ARG			ARG	ARG	THR	THR	THR	THR	THR	THR	ARG	ARG
310	293	290	GLU	ASP	ASP	GLU	GLU	GLU				GLU	GLU	ALA	ALA	ALA	ALA	ALA	ALA	ASP	ASP
311	294	291	GLU	LEU	LEU	GLU	GLU	GLU				GLU	GLU	SER	SER	SER	SER	SER	SER	LEU	LEU
312	295	292	GLN	CYS	CYS	GLN	GLN	GLN				GLN	GLN	THR	THR	THR	ALA	THR	THR	CYS	CYS
313	296	293	TYR	GLY	GLY	TYR	PHE	PHE				PHE	PHE	THR	THR	THR	THR	THR	GLU	GLY	GLY
314	297	294	ASN	CYS	CYS	ASN	ASN	ASN				ASN	ASX	GLN	GLN	GLN	GLN	GLN	SER	CYS	CYS
315		295	---	---	---	---	---	---				---	---	GLU	GLU	GLU	GLU	GLU	GLU	---	---
316		296	---	---	---	---	---	---				---	---	GLY	GLY	GLY	GLY	GLY	GLY	---	---
317	298	297	SER	---	---	SER	SER	SER				SER	SER	GLU	GLU	GLU	GLU	GLU	GLU	---	---
318	299	298	THR	---	---	THR	THR	THR				THR	THR	LEU	LEU	LEU	LEU	LEU	LEU	---	---
319	300	299	TYR	TYR	TYR	TYR	PHE	PHE	PHE			TYR	TYR	ALA	ALA	ALA	ALA	ALA	ALA	TYR	TYR
320	301	300	ARG	SER	SER	HIS	ARG	ARG	ARG			ARG	ARG	SER	SER	SER	SER	SER	SER	SER	SER
321	302	301	VAL	VAL	VAL	VAL	VAL	VAL	VAL			VAL	VAL	THR	THR	THR	THR	THR	THR	VAL	VAL
322	303	302	VAL	SER	SER	VAL	VAL	VAL	VAL			VAL	VAL	GLN	GLN	GLN	GLN	GLN	GLU	SER	SER
323	304	303	SER	SER	SER	SER	SER	SER	SER			SER		SER	SER	SER	SER	SER	SER	SER	SER
324	305	304	VAL	VAL	VAL	VAL	VAL	VAL	VAL			VAL		GLU	GLU	GLU	GLU	GLU	GLU	VAL	VAL
325	306	305	LEU	LEU	LEU	LEU	LEU	LEU	LEU			LEU		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
326	307	306	THR	PRO	PRO	THR	THR	THR	THR			THR		THR	THR	THR	THR	THR	THR	PRO	PRO
327	308	307	VAL	GLY	GLY	VAL	VAL	VAL	VAL			VAL		LEU	LEU	LEU	LEU	LEU	LEU	GLY	GLY
328	309	308	LEU	CYS	CYS	VAL	VAL	VAL	VAL			LEU		SER	SER	SER	SER	SER	SER	CYS	CYS
329	310	309	HIS	ALA	ALA	HIS	HIS	HIS	HIS			HIS		GLN	GLN	GLN	GLN	GLN	GLN	ALA	ALA
330	311	310	GLN	GLU	GLU	GLN	GLN	GLN	GLN			GLN		LYS	LYS	LYS	LYS	LYS	GLX	GLX	GLX
331	312	311	ASP	PRO	PRO	ASN	ASP	ASP	ASP			ASP		HIS	HIS	HIS	ARG	HIS	HIS	PRO	PRO
332	313	312	TRP	TRP	TRP	TRP	TRP	TRP	TRP			TRP		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
333	314	313	LEU	ASN	ASN	LEU	LEU	LEU	LEU			LEU		LEU	LEU	LEU	LEU	LEU	LEU	ASN	ASN
			---	---	---	---	---	---	---			---		---	---	---	---	---	---	---	---
			---	---	---	---	---	---	---			---		---	---	---	---	---	---	---	---
334	315	314	ASN	HIS	HIS	ASN	ASN	ASP	ASP			ASN		SER	SER	SER	SER	SER	SER	HIS	HIS
335	316	315	GLY	GLY	GLY	GLY	GLY	GLY	GLY			GLY		ASP	ASP	ASP	ASP	ASP	ASP	GLY	GLY
336	317	316	LYS	LYS	LYS	LYS	LYS	LYS	LYS			LYS	LYS	ARG	ARG	ARG	ARG	ARG	ARG	GLU	GLU
337	318	317	GLU	THR	THR	GLU	GLU	GLU	GLN			GLU	GLU	THR	THR	THR	THR	THR	THR	THR	THR
338	319	318	TYR	PHE	PHE	TYR	TYR	TYR	TYR			TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	PHE	PHE
339	320	319	LYS	THR	THR	LYS	LYS	LYS	LYS			LYS	LYS	THR	THR	THR	THR	THR	THR	THR	THR
340	321	320	CYS	CYS	CYS	CYS	CYS	CYS	CYS			CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
341	322	321	LYS	THR	THR	LYS	LYS	LYS	LYS			LYS	LYS	GLN	GLN	GLN	GLN	GLN	GLU	THR	THR
342	323	322	VAL	ALA	ALA	VAL	VAL	VAL	VAL			VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ALA	ALA
343	324	323	SER	ALA	ALA	SER	SER	SER	SER			SER	SER	THR	THR	THR	THR	THR	THR	ALA	ALA
344	325	324	ASN	TYR	TYR	ASN	ASN	ASN	ASN			ASN	ASN	TYR	TYR	TYR	TYR	TYR	TYR	HIS	HIS
345	326	325	LYS	PRO	PRO	LYS	LYS	LYS	LYS			LYS	LYS	GLN	GLN	GLN	GLN	GLN	GLX	PRO	PRO
346	327	326	ALA	GLU	GLU	GLY	GLY	GLY	GLY			GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLU	GLU	GLU
347	328	327	LEU	SER	SER	LEU	LEU	LEU	LEU			LEU	LEU	HIS	HIS	GLY	ASP	HIS	HIS	LEU	LEU
348	329	328	PRO	LYS	LYS	PRO	PRO	PRO	PRO			PRO	PRO	THR	THR	THR	THR	THR	THR	LYS	LYS
349	330	329	ALA	THR	THR	ALA	ALA	ALA	ALA			SER	SER	PHE	PHE	PHE	PHE	PHE	PHE	THR	THR
350	331	330	PRO	PRO	PRO	PRO	PRO	PRO	PRO			SER	SER	GLU	GLU	GLU	GLU	GLU	GLX	PRO	PRO
351	332	331	ILE	LEU	LEU	ILE	ILE	ILE	ILE			ILE	ILE	---	---	---	---	---	---	LEU	LEU
351A			---	---	---	---	---	---	---			---	---	---	---	---	---	---	---	---	---
352	333	332	GLU	THR	THR	GLU	GLU	GLU	GLU			GLU	GLU	ASP	ASP	ASP	ASP	ASP	ASX	THR	THR
353	334	333	LYS	ALA	ALA	LYS	LYS	LYS	LYS		LYS	LYS	LYS	SER	SER	SER	SER	SER	SER	ALA	ALA
354	335	334	THR	THR	THR	THR	THR	THR	THR		THR	THR	THR	THR	THR	THR	THR	THR	THR	ASN	ASN
355	336	335	ILE	LEU	LEU	ILE	ILE	ILE	ILE		ILE	ILE	ILE	LYS	LYS	LYS	LYS	LYS	LYS	ILE	ILE
356		336	---	---	---	---	---	---	---		---	---	---	LYS	LYS	LYS	LYS	LYS	LYS	---	---
357	337	337	SER	SER	SER	SER	SER	SER	SER		SER	SER	SER	CYS	CYS	CYS	CYS	CYS	CYS	THR	THR
358	338	338	LYS	LYS	LYS	LYS	LYS	LYS	LYS		LYS	LYS	LYS	ALA	ALA	ALA	ALA	ALA	ALA	LYS	LYS
359	339	339	ALA	---	---	THR	THR	THR	THR		THR	ALA	ALA	---	---	---	---	---	---	SER	SER
360	340		LYS	SER	SER	LYS	LYS	LYS	LYS		LYS	LYS	LYS	---	---	---	---	---	---	---	---

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

EU INDEX	OU INDEX	63 HUMAN IGA2 'CL	64 HUMAN IGA2 A2M(1) 'CL	65 HUMAN IGA2 A2M(2) 'CL	66 IGM 'CL ϕ	67 IGM 'CL' ϕ	68 IGM-b 'CL	69 MUTANT 102 'CL ϕ	70 MOPC 104E	71 MOPC 104E MEMB 'CL ϕ	72 HPC76 'CL ϕ	73 G8 CA 1.7 'CL	74 GAT50 'CL	75 IGD 'CL ϕ	76 IGD SECR 'CL ϕ	77 IGD MEMB 'CL ϕ	78 B1-8. DELTA1	79 MOUSE IGG3 'CL	80 IGG3 MEMB 'CL
243A			---		---	---	---		---		---			---				---	
243B			---		---	---	---		---		---			---				---	
243C			---		---	---	---		---		---			---				---	
243D			---		---	---	---		---		---			---				---	
243E			---		---	---	---		---		---			---				---	
243F			---		---	---	---		---		---			---				---	
243G	230		---		ALA	ALA	ALA		ALA		ALA			---				---	
243H	231		---		VAL	VAL	VAL		VAL		VAL			---				---	
243I	232		---		ALA	ALA	ALA		ALA		ALA			---				---	
244	231		---		---	---	---		---		---			---				---	
245	232		---		---	---	---		---		---			---				PRO	
245A			---		---	---	---		---		---			---				GLY	
245B			---		---	---	---		---		---			---				---	
245C			VAL		---	---	---		---		---			---				---	
246	233	233	PRO		GLU	GLU	GLU		GLU		GLU			---				---	
247	234	234	PRO		MET	MET	MET		MET		MET			---				ASN	
248	235	235	PRO		ASN	ASN	ASN		ASN		ASN			---				ILE	
249	236	236	PRO		PRO	PRO	PRO		PRO		PRO			---				LEU	
250	237	237	PRO		ASN	ASN	ASN		ASN		ASN			---				GLY	
251	238	238	CYS		VAL	VAL	VAL		VAL		VAL			---				GLY	
251A			CYS		---	---	---		---		---			---				PRO	
251B			HIS		---	---	---		---		---			---				---	
252	239	239	PRO		ASN	ASN	ASN		ASN		ASN			---				---	
253	240	240	ARG		VAL	VAL	VAL		VAL		VAL			---				SER	
254	241	241	LEU		PHE	PHE	PHE		PHE		PHE			---				VAL	
255	242	242	SER		VAL	VAL	VAL		VAL		VAL			---				PHE	
256	243		LEU		---	---	---		---		---			---				ILE	
257	244	243	HIS		PRO	PRO	PRO		PRO		PRO			---				PHE	
258	245	244	ARG		PRO	PRO	PRO		PRO		PRO			---				PRO	
259	246	245	PRO		ARG	ARG	ARG		ARG		ARG			---				PRO	
260	247	246	ALA		ASP	ASP	ASP		ASP		ASP			---				LYS	
261	248	247 LEU	LEU	LEU	GLY	GLY	GLY		GLY		GLY			---				PRO	
262	249	248 GLU	GLU	GLU	PHE	PHE	PHE		PHE		PHE			---				LYS	
263	250	ASP	ASP	ASP	SER	SER	SER		SER		SER			---				ASP	
264	251	249 LEU	LEU	LEU	GLY	GLY	GLY		GLY		GLY			---				ALA	
265	252	250 LEU	LEU	LEU	PRO	PRO	PRO		PRO		PRO			---				LEU	
266	253	251 LEU	LEU	LEU	ALA	ALA	ALA		ALA		ALA			---				MET	
267	254	252 GLY	GLY	GLY	PRO	PRO	PRO		PRO		PRO			---				ILE	
268	255	253 SER	SER	SER	ARG	ARG	ARG		ARG		ARG			---				SER	
269	256	254 GLU	GLU	GLU	LYS	LYS	LYS		LYS		LYS			---				LEU	
270	257	255 ALA	ALA	ALA	SER	SER	SER		SER		SER			---				THR	
271	258	256 ASN	ASN	ASN	LYS	LYS	LYS		LYS		LYS			---				PRO	
272	259	257 LEU	LEU	LEU	LEU	LEU	LEU		LEU		LEU			---				LYS	
273	260	258 THR	THR	THR	ILE	ILE	ILE		ILE		ILE			---				VAL	
274	261	259 CYS	CYS	CYS	CYS	CYS	CYS		CYS		CYS			---				THR	
275	262	260 THR	THR	THR	GLU	GLU	GLU		GLU		GLU			---				CYS	
276	263	261 LEU	LEU	LEU	ALA	ALA	ALA		ALA		ALA			---				VAL	
277	264	262 THR	THR	THR	THR	THR	THR		THR		THR			---				VAL	
278	265	263 GLY	GLY	GLY	ASN	ASN	ASN		ASN		ASN			---				VAL	
279	266	264 LEU	LEU	LEU	PHE	PHE	PHE		PHE		PHE			---				ASP	
280	267	265 ARG	ARG	ARG	THR	THR	THR		THR		THR			---				VAL	
281	268	266 ASP	ASP	ASP	PRO	PRO	PRO		PRO		PRO			---				SER	
282	269	267 ALA	ALA	ALA	LYS	LYS	LYS		LYS		LYS			---				GLU	
283	270	268 SER	SER	SER	PRO	PRO	PRO		PRO		PRO			---				ASP	
284	271	---	---	---	ILE	ILE	ILE		ILE		ILE			---				ASP	
285	272	GLY	GLY	GLY	THR	THR	THR		THR		THR			---				PRO	
286	273	269 ALA	ALA	ALA	VAL	VAL	VAL		VAL		VAL			---				ASP	
287	274	THR	THR	THR	---	---	---		---		---			---				VAL	
288	275	PHE	PHE	PHE	---	---	---		---		---			---				HIS	
289	276	270 THR	THR	THR	SER	SER	SER		SER		SER			---				VAL	
290	277	271 TRP	TRP	TRP	TRP	TRP	TRP		TRP		TRP			---				SER	
291	278	272 ---	THR	THR	LEU	LEU	LEU		LEU		LEU			---				TRP	
292	279	273 ---	PRO	PRO	LYS	LYS	LYS		LYS		LYS			---				PHE	
293		274 THR	---	---	ASP	ASP	ASP		ASP		ASP			---				VAL	
294		275 PRO	---	---	GLY	GLY	GLY		GLY		GLY			---				---	
295	280	276 SER	---	---	LYS	LYS	LYS		LYS		LYS			---				---	
296	281	277 SER	SER	SER	LEU	LEU	LEU		LEU		LEU			---				ASP	
297		278 ---	---	---	VAL	VAL	VAL		VAL		VAL			---				ASN	
298		279 ---	SER	SER	GLU	GLU	GLU		GLU		GLU			---				---	
299	282	280 GLY	GLY	GLY	SER	SER	SER		SER		SER			---				---	
300	283	281 LYS	LYS	LYS	GLY	GLY	GLY		GLY		GLY			---				LYS	
301	284	282 SER	SER	SER	PHE	PHE	PHE		PHE		PHE			---				GLU	
302	285	283 ALA	ALA	ALA	THR	THR	THR		THR		THR			---				VAL	
303	286	VAL	VAL	VAL	---	---	---		---		---			---				HIS	
304	287	284 GLN	GLN	GLN	THR	THR	THR		THR		THR			---				THR	
305	288	285 GLY	GLY	GLY	ASP	ASP	ASP		ASP		ASP			---				ALA	
306	289	286 PRO	PRO	PRO	PRO	PRO	PRO		PRO		PRO			---				TRP	
307	290	287 PRO	PRO	PRO	VAL	VAL	VAL		VAL		VAL			---				THR	
308	291	288 GLU	GLU	GLU	THR	THR	THR		THR		THR			---				GLN	
309	292	289 ARG	ARG	ARG	ILE	ILE	ILE		ILE		ILE			---				PRO	
310	293	290 ASP	ASP	ASP	GLU	GLU	GLU		GLU		GLU			---				ARG	
311	294	291 LEU	LEU	LEU	ASN	ASN	ASN		ASN		ASN			---				GLU	
312	295	292 CYS	CYS	CYS	LYS	LYS	LYS		LYS		LYS			---				ALA	
313	296	293 GLY	GLY	GLY	GLY	GLY	GLY		GLY		GLY			---				GLN	
314	297	294 CYS	CYS	CYS	SER	SER	SER		SER		SER			---				TYR	
315		295 ---	---	---	THR	THR	THR		THR		THR			---				---	
316		296 ---	---	---	PRO	PRO	PRO		PRO		PRO			---				ASN	
317	298	297 ---	---	---	GLN	GLN	GLN		GLN		GLN			---				---	
318	299	298 ---	---	---	THR	THR	THR		THR		THR			---				---	
319	300	299 TYR	TYR	TYR	TYR	TYR	TYR		TYR		TYR			---				SER	
320	301	300 SER	SER	SER	LYS	LYS	LYS		LYS		LYS			---				THR	
321	302	301 VAL	VAL	VAL	VAL	VAL	VAL		VAL		VAL			---				PHE	
322	303	302 SER	SER	SER	ILE	ILE	ILE		ILE		ILE			---				ARG	
323	304	303 **SER**	**SER**	**SER**	**SER**	**SER**	**SER**		**SER**		**SER**			---				VAL	
324	305	304 VAL	VAL	VAL	THR	THR	THR		THR		THR			---				VAL	
325	306	305 LEU	LEU	LEU	LEU	LEU	LEU		LEU		LEU			---				**SER**	
326	307	306 PRO	PRO	PRO	THR	THR	THR		THR		THR			---				ALA	
327	308	307 GLY	GLY	GLY	ILE	ILE	ILE		ILE		ILE			---				LEU	
328	309	308 CYS	CYS	CYS	SER	SER	SER		SER		SER			---				PRO	
329	310	309 ALA	ALA	ALA	GLU	GLU	GLU		GLU		GLU			---				ILE	
330	311	310 GLN	GLN	GLN	ILE	ILE	ILE		ILE		ILE			---				GLN	
331	312	311 PRO	PRO	PRO	ASP	ASP	ASP		ASP		ASP			---				HIS	
332	313	312 **TRP**	**TRP**	**TRP**	**TRP**	**TRP**	**TRP**		**TRP**		**TRP**			---				GLN	
333	314	313 ASN	ASN	ASN	LEU	LEU	LEU		LEU		LEU			---				ASP	
		---	---	---	---	---	---		---		---			---				**TRP**	
		---	---	---	---	---	---		---		---			---				MET	
334	315	314 HIS	HIS	HIS	ASN	ASN	ASN		ASN		ASN			---				---	
335	316	315 GLY	GLY	GLY	LEU	LEU	LEU		LEU		LEU			---				---	
336	317	316 GLU	GLU	GLU	ASN	ASN	ASN		ASN		ASN			---				ARG	
337	318	317 THR	THR	THR	VAL	VAL	VAL		VAL		VAL			---				GLY	
338	319	318 PHE	PHE	PHE	TYR	TYR	TYR		TYR		TYR			---				LYS	
339	320	319 THR	THR	THR	THR	THR	THR		THR		THR			---				GLU	
340	321	320 **CYS**	**CYS**	**CYS**	**CYS**	**CYS**	**CYS**		**CYS**		**CYS**			---				PHE	
341	322	321 THR	THR	THR	ARG	ARG	ARG		ARG		ARG			---				LYS	
342	323	322 ALA	ALA	ALA	VAL	VAL	VAL		VAL		VAL			---				**CYS**	
343	324	323 ALA	ALA	ALA	ASP	ASP	ASP		ASP		ASP			---				LYS	
344	325	324 HIS	HIS	HIS	HIS	HIS	HIS		HIS		HIS			---				VAL	
345	326	325 PRO	PRO	PRO	ARG	ARG	ARG		ARG		ARG			---				ASN	
346	327	326 GLU	GLU	GLU	GLY	GLY	GLY		GLY		GLY			---				ASN	
347	328	327 LEU	LEU	LEU	LEU	LEU	LEU		LEU		LEU			---				LYS	
348	329	328 LYS	LYS	LYS	THR	THR	THR		THR		THR			---				ALA	
349	330	329 THR	THR	THR	PHE	PHE	PHE		PHE		PHE			---				LEU	
350	331	330 PRO	PRO	PRO	LEU	LEU	LEU		LEU		LEU			---				PRO	
351	332	331 LEU	LEU	LEU	LYS	LYS	LYS		LYS		LYS			---				ALA	
351A		---	---	---	---	---	---		---		---			---				PRO	
352	333	332 THR	THR	THR	ASN	ASN	ASN		ASN		ASN			---				ILE	
353	334	333 ALA	ALA	ALA	VAL	VAL	VAL		VAL		VAL			---				---	
354	335	334 ASN	ASN	ASN	SER	SER	SER		SER		SER			---				GLU	
355	336	335 ILE	ILE	ILE	SER	SER	SER		SER		SER			---				ARG	
356		336 ---	---	---	THR	THR	THR		THR		THR			---				THR	
357	337	337 THR	THR	THR	CYS	CYS	CYS		CYS		CYS			---				ILE	
358	338	338 LYS	LYS	LYS	ALA	ALA	ALA		ALA		ALA			---				---	
359	339	339 SER	---	---	ALA	ALA	ALA		ALA		ALA			---				SER	
360	340	---	SER	SER	---	---	---		---		---			---				LYS	
																		PRO	
																		LYS	

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

	EU INDEX	OU INDEX	81 IGG1 'CL #	82 IGG1 MEMB 'CL #	83 MOPC 21 #	84 IF2 'CL #	85 ICR 11.19.3	86 IGG2B (A) 'CL #	87 IGG2B (A) 'CL' #	88 IGG2B (B) 'CL #	89 IGG2B MEMB 'CL #	90 MPC 11 #	91 10.1 #	92 IGG2A (A) 'CL #	93 17/9 'CL #	94 IGG2A (B) 'CL #	95 IGG2A (B) 'CL' #	96 IGG2A MEMB 'CL #	97 MOPC 173 #	98 CBPC 101 #	99 IGA 'CL #
243A			---		---	---		---	---	---			---	---	---	---	---		---	---	---
243B			---		---	---		---	---	---			---	---	---	---	---		---	---	---
243C			---		---	---		---	---	---			---	---	---	---	---		---	---	---
243D			---		---	---		---	---	---			---	---	---	---	---		---	---	---
243E			---		---	---		---	---	---			---	---	---	---	---		---	---	---
243F			---		---	---		---	---	---			---	---	---	---	---		---	---	---
243G		230	---		---	---		---	---	---			---	---	---	---	---		---	---	---
243H		231	---		---	---		---	---	---			---	---	---	---	---		---	---	---
243I		232	---		---	---		---	---	---			---	---	---	---	---		---	---	GLY
244	231		VAL		VAL	VAL		ALA	ALA	ALA			ALA	ALA	ALA	ALA	ALA		ALA	ALA	PRO
245	232		PRO		PRO	PRO		PRO	PRO	PRO			PRO	PRO	PRO	PRO	PRO		PRO	PRO	THR
245A			---		---			---	---	---			---	---	---	---	---		---	---	PRO
245B			---		---			---	---	---			---	---	---	---	---		---	---	PRO
245C			---		---			---	---	---			---	---	---	---	---		---	---	PRO
246	233	233	---		---			ASN	ASN	ASN			ASN	ASN	ASN	ASP	ASP		ASN	ASP	PRO
247	234	234	---		---		LEU	LEU	LEU	LEU		LEU	LEU	LEU	LEU	LEU	LEU		LEU	LEU	ILE
248	235	235	---		---		GLU	GLU	GLU	GLU		GLU	GLU	LEU	LEU	LEU	LEU		LEU	LEU	THR
249	236	236	GLU		GLU		GLY	GLY	GLY	GLY		GLY	GLY	GLY	GLY	GLY	GLY		GLY	GLY	ILE
250	237	237	VAL		VAL		GLY	GLY	GLY	GLY		GLY	GLY	GLY		GLY	GLY		GLY	GLY	PRO
251	238	238	SER		SER		PRO	PRO	PRO	PRO		PRO	PRO	PRO		PRO	PRO		PRO	PRO	SER
251A			---		---		---	---	---	---		---	---	---		---	---		---	---	CYS
251B			---		---		---	---	---	---		---	---	---		---	---		---	---	GLN
252	239	239	SER		SER		SER	SER	SER	SER		SER	SER	SER		SER	SER		SER	SER	PRO
253	240	240	VAL		VAL		VAL	VAL	VAL	VAL		VAL	VAL	VAL		VAL	VAL		VAL	VAL	SER
254	241	241	PHE		PHE		PHE	PHE	PHE	PHE		PHE	PHE	PHE		PHE	PHE		PHE	PHE	LEU
255	242	242	ILE		ILE		ILE	ILE	ILE	ILE		ILE	ILE	ILE		ILE	ILE		ILE	ILE	SER
256	243		PHE		PHE		PHE	PHE	PHE	PHE		PHE	PHE	PHE		PHE	PHE		PHE	PHE	LEU
257	244	243	PRO		PRO		PRO	PRO	PRO	PRO		PRO	PRO	PRO		PRO	PRO		PRO	PRO	GLN
258	245	244	PRO		PRO		PRO	PRO	PRO	PRO		PRO	PRO	PRO		PRO	PRO		PRO	PRO	ARG
259	246	245	LYS		LYS		ASN	ASN	ASN	ASN		ASN	ASN	LYS		LYS	LYS		LYS	LYS	PRO
260	247	246	PRO		PRO		ILE	ILE	ILE	ILE		ILE	ILE	ILE		ILE	ILE		ILE	ILE	ALA
261	248	247	LYS		LYS		LYS	LYS	LYS	LYS		LYS	LYS	LYS		LYS	LYS		LYS	LYS	LEU
262	249	248	ASP		ASP		ASP	ASP	ASP	ASP		ASP	ASP	ASP		ASP	ASP		ASN	ASP	GLU
263	250		VAL		THR		VAL	VAL	VAL	VAL		VAL	VAL	VAL		VAL	VAL		VAL	VAL	ASP
264	251	249	LEU		LEU		LEU	LEU	LEU	LEU		LEU	LEU	LEU		LEU	LEU		LEU	LEU	LEU
265	252	250	THR		LEU		MET	MET	MET	MET		MET	MET	MET		MET	MET		MET	MET	LEU
266	253	251	ILE		ILE		ILE	ILE	ILE	ILE		ILE		ILE		ILE	ILE		ILE	ILE	LEU
267	254	252	THR		THR		SER	SER	SER	SER		SER		SER		SER	SER		SER	SER	GLY
268	255	253	LEU		VAL		LEU	LEU	LEU	LEU		LEU		LEU		LEU	LEU		LEU	LEU	SER
269	256	254	THR		THR		THR	THR	THR	THR		THR		SER		SER	SER		SER	SER	ASP
270	257	255	PRO		PRO		PRO	PRO	PRO	PRO		PRO		PRO		PRO	PRO		PRO	PRO	ALA
271	258	256	LYS		LYS		LYS	LYS	LYS	LYS		LYS		ILE		MET	MET		ILE	MET	SER
272	259	257	VAL		VAL		VAL	VAL	VAL	VAL		VAL		VAL		LEU	VAL		VAL	VAL	ILE
273	260	258	THR		THR		THR	THR	THR	THR		THR		THR		THR	THR		THR	THR	THR
274	261	259	CYS		CYS		CYS	CYS	CYS	CYS		CYS		CYS		CYS	CYS		CYS	CYS	CYS
275	262	260	VAL		VAL		VAL	VAL	VAL	VAL		VAL		VAL		VAL	VAL		VAL	VAL	THR
276	263	261	VAL		VAL		VAL	VAL	VAL	VAL		VAL		VAL		VAL	VAL		VAL	VAL	LEU
277	264	262	VAL		VAL		VAL	VAL	VAL	VAL		VAL		VAL		VAL	VAL		VAL	VAL	ASN
278	265	263	ASP		ASP		ASP	ASP	ASP	ASP		ASP		ASP		ASP	ASP		ASP	ASP	GLY
279	266	264	ILE		ILE		VAL	VAL	VAL	VAL		VAL		VAL		VAL	VAL		VAL	VAL	LEU
280	267	265	SER		SER			SER	SER	SER				SER		SER	SER		SER	SER	ARG
281	268	266	LYS		LYS		GLU	GLU	GLU	GLU		GLU		GLU		GLU	GLU		GLU	GLU	ASN
282	269	267	ASP		ASP		ASP	ASP	ASP	ASP		ASP		ASP		ASP	ASP		ASP	ASP	PRO
283	270	268	ASP		ASP		ASP	ASP	ASP	ASP		ASP		ASP		ASP	ASP		ASP	ASP	GLU
284	271		PRO		PRO			PRO	PRO	PRO		PRO		PRO		PRO	PRO		PRO	PRO	GLY
285	272		GLU		GLU			ASP	ASP	ASP		ASP		ASP		ASP	ASP		ASP	ASP	ALA
286	273	269	VAL		VAL		VAL	VAL	VAL	VAL		VAL		VAL		VAL	VAL		VAL	VAL	VAL
287	274		GLN		GLN		GLN	GLN	GLN	ARG		GLN		GLN		GLN	GLN		GLN	GLN	---
288	275		PHE		PHE		ILE	ILE	ILE	ILE		ILE		ILE		ILE	ILE		ILE	ILE	PHE
289	276	270	SER		SER			SER	SER	SER				SER		SER	SER		SER	SER	THR
290	277	271	TRP		TRP			TRP	TRP	TRP				TRP		TRP	TRP		TRP	TRP	TRP
291	278	272	PHE		PHE			PHE	PHE	PHE		PHE		PHE		PHE	PHE		PHE	PHE	GLU
292	279	273	VAL		VAL			VAL	VAL	VAL		VAL		VAL		VAL	VAL		VAL	VAL	PRO
293		274	---		---			---	---	---				---		---	---		---	---	---
294		275	---		---			---	---	---				---		---	---		---	---	---
295	280	276	ASP		ASP			ASN	ASN	ASN				ASN		ASN	ASN		ASP	ASN	SER
296	281	277	ASP		ASN			ASN	ASN	ASN				ASN		ASN	ASN		ASN	ASN	THR
297		278	---		---			---	---	---				---		---	---		---	---	---
298		279	---		---			---	---	---				---		---	---		---	---	---
299	282	280	VAL		VAL			VAL	VAL	VAL				VAL		VAL	VAL		VAL	VAL	GLY
300	283	281	GLU		GLU			GLU	GLU	GLU				GLU		GLU	GLU		GLU	GLU	LYS
301	284	282	VAL		VAL			VAL	VAL	VAL				VAL		VAL	VAL		VAL	VAL	ASP
302	285	283	HIS		HIS			HIS	HIS	HIS				HIS		HIS	HIS		HIS	HIS	ALA
303	286		THR		THR			THR	THR	THR				THR		THR	THR		GLN	THR	VAL
304	287	284	ALA		ALA			ALA	ALA	ALA				ALA		ALA	ALA		ALA	ALA	GLN
305	288	285	GLN		GLN			GLN	GLN	GLN				GLN		GLN	GLN		GLN	GLN	LYS
306	289	286	THR		THR			THR	THR	THR				THR		THR	THR		THR	THR	LYS
307	290	287	GLN		GLN			GLN	GLN	GLN				GLN		GLN	GLN		THR	GLN	ALA
308	291	288	PRO		PRO			THR	THR	THR				THR		THR	THR		HIS	THR	VAL
309	292	289	ARG		ARG			HIS	HIS	HIS				HIS		HIS	HIS		THR	HIS	GLN
310	293	290	GLU		GLU			ARG	ARG	ARG				ARG		ARG	ARG		ARG	ARG	ASN
311	294	291	GLU		GLU			GLU	GLU	GLU				GLU		GLU	GLU		GLN	GLU	SER
312	295	292	GLN		GLN			ASP	ASP	ASP				ASP		ASP	ASP		ASN	ASP	CYS
313	296	293	PHE		PHE			TYR	TYR	TYR				TYR		TYR	TYR		TYR	TYR	GLY
314	297	294	ASN		ASX			ASN	ASN	ASN				ASN		ASN	ASN		ASX	ASN	CYS
315		295	---		---			---	---	---				---		---	---		---	---	---
316		296	---		---			---	---	---				---		---	---		---	---	---
317	298	297	SER		SER			SER	SER	SER				SER		SER	SER		SER	SER	---
318	299	298	THR		THR			THR	THR	THR				THR		THR	THR		THR	THR	---
319	300	299	PHE		PHE			ILE	ILE	ILE				LEU		LEU	LEU		LEU	LEU	TYR
320	301	300	ARG		ARG			ARG	ARG	ARG				ARG		ARG	ARG		ARG	ARG	SER
321	302	301	SER		VAL			VAL	VAL	VAL				VAL		VAL	VAL		VAL	VAL	VAL
322	303	302	VAL		VAL			VAL	VAL	VAL				VAL		VAL	VAL		VAL	VAL	SER
323	304	303	SER		SER			SER	SER	SER				SER		SER	SER		SER	SER	SER
324	305	304	GLU		ALA			THR	THR	ALA				ALA		ALA	ALA		ALA	ALA	VAL
325	306	305	LEU		LEU			LEU	LEU	LEU				LEU		LEU	LEU		LEU	LEU	LEU
326	307	306	PRO		PRO			PRO	PRO	PRO				PRO		PRO	PRO		PRO	PRO	PRO
327	308	307	ILE		ILE			ILE	ILE	ILE				ILE		ILE	ILE		ILE	ILE	GLY
328	309	308	MET		MET			GLN	GLN	GLN				GLN		GLN	GLN		GLN	GLN	CYS
329	310	309	HIS		HIS			HIS	HIS	HIS				HIS		HIS	HIS		HIS	HIS	ALA
330	311	310	GLN		GLN			GLN	GLN	GLN				GLN		GLN	GLN		GLN	GLN	GLU
331	312	311	ASP		ASP			ASP	ASP	ASP				ASP		ASP	ASP		ASN	ASP	ARG
332	313	312	TRP		TRP			TRP	TRP	TRP				TRP		TRP	TRP		TRP	TRP	TRP
333	314	313	LEU		LEU			MET	MET	MET				MET		MET	MET		MET	MET	ASN
			---		---			---	---	---				---		---	---		---	---	---
			---		---			---	---	---				---		---	---		---	---	---
334	315	314	ASN		ASN		SER	SER	SER	SER		SER		SER		SER	SER		SER	SER	SER
335	316	315	GLY		GLY		GLY	GLY	GLY	GLY		GLY		GLY		GLY	GLY		GLY	GLY	GLY
336	317	316	LYS		LYS		LYS	LYS	LYS	LYS		LYS		LYS		LYS	LYS		LYS	LYS	ALA
337	318	317	GLU		GLU		GLU	GLU	GLU	GLU		GLU		GLU		GLU	GLU		GLU	GLU	SER
338	319	318	PHE		PHE		PHE	PHE	PHE	PHE		PHE		PHE		PHE	PHE		PHE	PHE	PHE
339	320	319	LYS		LYS		LYS	LYS	LYS	LYS		LYS		LYS		LYS	LYS		LYS	LYS	LYS
340	321	320	CYS		CYS		CYS	CYS	CYS	CYS		CYS		CYS		CYS	CYS		CYS	CYS	CYS
341	322	321	ARG		ARG		LYS	LYS	LYS	LYS		LYS		LYS		LYS	LYS		LYS	LYS	THR
342	323	322	VAL		VAL		VAL	VAL	VAL	VAL		VAL		VAL		VAL	VAL		VAL	VAL	VAL
343	324	323	ASN		ASN		ASN	ASN	ASN	ASN		ASN		ASN		ASN	ASN		ASN	ASN	THR
344	325	324	SER		SER		ASN	ASN	ASN	ASN		ASN		ASN		ASN	ASN		ASN	ASN	HIS
345	326	325	ALA		ALA		LYS	LYS	LYS	LYS		LYS		LYS		ARG	ARG		LYS	ARG	PRO
346	327	326	ALA		ALA		ASP	ASP	ASP	ASP		ASP		ASP		ALA	ALA		ASP	ALA	GLU
347	328	327	PHE		PHE		LEU	LEU	LEU	LEU		LEU		LEU		LEU	LEU		LEU	LEU	SER
348	329	328	PRO		PRO		PRO	PRO	PRO	PRO		PRO		PRO		PRO	PRO		PRO	PRO	GLY
349	330	329	ALA		ALA		ALA	SER	SER	SER		SER		ALA		SER	SER		ALA	SER	THR
350	331	330	PRO		PRO		PRO	PRO	PRO	PRO		PRO		PRO		PRO	PRO		PRO	PRO	---
351	332	331	ILE		ILE		ILE	ILE	ILE	ILE		ILE		ILE		ILE	ILE		ILE	ILE	LEU
351A			---		---		---	---	---	---		---		---		---	---		---	---	---
352	333	332	GLU		GLU		GLU	GLU	GLU	GLU		GLU		GLU		GLU	GLU		GLU	GLU	THR
353	334	333	LYS		LYS		ARG	ARG	ARG	ARG		ARG		ARG		LYS	LYS		ARG	LYS	GLY
354	335	334	THR		THR		THR	THR	THR	THR		THR		THR		THR	THR		THR	THR	THR
355	336	335	ILE		ILE		ILE	ILE	ILE	ILE		ILE		ILE		ILE	ILE		ILE	ILE	ILE
356		336	---		---		---	---	---	---		---		---		---	---		---	---	---
357	337	337	SER		SER		SER	SER	SER	SER				SER		SER	SER		SER	SER	ALA
358	338	338	LYS		LYS		LYS	LYS	LYS	LYS		LYS		LYS		LYS	LYS		LYS	LYS	LYS
359	339	339	THR		THR		PRO	ILE	ILE	ILE		ILE		PRO		PRO	PRO		PRO	PRO	VAL
360	340		LYS		LYS		LYS	LYS	LYS	LYS		LYS		LYS		ARG	ARG		LYS	ARG	THR

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

EU INDEX	OU INDEX	100 IGA 'CL' #	101 MOPC 47A	102 MOPC 315	103 MOPC 511 #	104 IGE 'CL #	105 IGE 'CL'	106 IGE a 'CL #	107 IGE b 'CL #	108 IGE MEMB 'CL #	109 IGA MEMB 'CL	110 RAT IGM 'CL	111 RAT IGD 'CL #	112 IR-731	113 RAT IGG2c 'CL	114 RAT IGG2a 'CL	115 RAT IGG1 'CL	116 RAT IGG2b 'CL	117 RAT IGA 'CL	118 RAT IGE 'CL	119 IRJ 'CL #	120 IR- 'CL #
243A		---	---		---	---	---	---	---					---	---	---	---	---		---	---	
243B		---	---		---	---	---	---	---					---	---	---	---	---		---	---	
243C		---	---		---	---	---	---	---					---	---	---	---	---		---	---	
243D		---	---		---	---	---	---	---					---	---	---	---	---		---	---	
243E		---	---		---	---	---	---	---					---	---	---	---	---		---	---	
243F		---	---		---	---	---	---	---					---	---	---	---	---		---	---	
243G	230	---	---		---	VAL	VAL	VAL	VAL					---	---	---	---	---		---	---	
243H	231	---	---		---	ARG	ARG	ARG	ARG					---	---	---	---	---		ALA	ALA	
243I	232	GLY	GLY		GLY	PRO	PRO	PRO	PRO			VAL		---	---	---	---	---		ARG	ARG	
244	231	PRO	PRO		PRO	---	---	---	---			VAL		---	---	---	---	---		PRO	PRO	
245	232	THR	THR		THR	---	---	---	---			---		VAL	---	---	---	VAL		---	---	
245A		PRO	PRO		PRO	---	---	---	---			---		GLY	ASP	---	---	---		---	---	
245B		PRO	PRO		PRO	---	---	---	---			---		---	---	---	---	PRO		---	---	
245C		PRO	PRO		PRO	---	---	---	---			---		---	---	---	---	---		---	---	
246	233	PRO	PRO		PRO	---	---	---	---			---		---	---	---	---	---		---	---	
247	234	ILE	ILE		ILE	VAL	VAL	VAL	VAL			---		---	---	---	---	---		---	---	
248	235	THR	THR		THR	THR	ASN	ASN	ASN			GLU		---	ASP	---	---	GLU		VAL	VAL	
249	236	ILE	ILE		ILE	HIS	ILE	ILE	ILE			MET		---	ASN	GLY	GLY	LEU		---	---	
250	237	PRO	PRO		GLY	SER	THR	THR	THR			ASN		---	LEU	SER	SER	LEU		ASN	ASN	
251	238	SER	SER		SER	LEU	GLU	GLU	GLU			PRO		---	GLY	GLU	GLU	GLY		ILE	ILE	
251A		CYS	CYS		CYS	SER	---	---	---			ASN		---	ARG	VAL	VAL	GLY		THR	THR	
251B		GLN	GLN		GLN	---	---	---	---			VAL		---	PRO	SER	SER	PRO		LYS	LYS	
252	239	PRO	PRO		PRO	PRO	PRO	PRO	PRO			---		---	---	---	---	---		---	---	
253	240	SER	SER		SER	PRO	THR	THR	THR			---		---	---	---	---	---		---	---	
254	241	LEU	LEU		LEU	TRP	LEU	LEU	LEU			SER		---	SER	SER	SER	SER		PRO	PRO	
255	242	SER	SER		SER	SER	GLU	GLU	GLU			VAL		---	VAL	VAL	VAL	VAL		THR	THR	
256	243	LEU	LEU		LEU	TYR	LEU	LEU	LEU			PHE		---	PHE	PHE	PHE	PHE		VAL	VAL	
257	244	GLN	GLN		GLN	SER	LEU	LEU	LEU			---		---	ILE	ILE	ILE	ILE		ASP	ASP	
258	245	ARG	ARG		ARG	ILE	HIS	HIS	HIS			PRO		---	PHE	PHE	PHE	PHE		LEU	LEU	
259	246	PRO	PRO		PRO	HIS	SER	SER	SER			PRO		---	PRO	PRO	PRO	PRO		LEU	LEU	
260	247	ALA	ALA		ALA	ARG	SER	SER	SER			PRO		---	PRO	PRO	PRO	PRO		HIS	HIS	
261	248	LEU	LEU		LEU	CYS	CYS	CYS	CYS			ARG		---	LYS	LYS	LYS	LYS		SER	SER	
262	249	GLU	GLU		GLU	ASP	ASP	ASP	ASP			ASP		---	PRO	THR	PRO	PRO		SER	SER	
263	250	ASP	ASP		ASP	PRO	PRO	PRO	PRO			ALA		---	LYS	LYS	LYS	LYS		CYS	CYS	
264	251	LEU	LEU		LEU	ASN	ASN	ASN	ASN			PHE		---	LYS	ASP	ASP	ASP		ASP	ASP	
265	252	LEU	LEU		LEU	ALA	ALA	ALA	ALA			SER		---	ILE	VAL	VAL	ILE		PRO	PRO	
266	253	LEU	LEU		LEU	PHE	PHE	PHE	ALA			GLY		---	LEU	LEU	LEU	LEU		ASN	ASN	
267	254	GLY	GLY		GLY	HIS	HIS	HIS	PHE			PRO		---	MET	THR	THR	LEU		ALA	ALA	
268	255	SER	SER		SER	SER	SER	SER	HIS			ALA		---	ILE	ILE	ILE	ILE		PHE	PHE	
269	256	ASP	ASP		ASP	THR	THR	THR	SER			PRO		---	THR	THR	THR	SER		HIS	HIS	
270	257	ALA	ALA		ALA	ILE	ILE	ILE	THR			ARG		---	LEU	LEU	LEU	GLN		SER	SER	
271	258	SER	GLN		GLN	GLN	GLN	GLN	ILE			LYS		---	THR	THR	THR	ASN		THR	THR	
272	259	ILE	ILE		ILE	LEU	LEU	LEU	GLN			SER		---	PRO	PRO	PRO	ALA		ILE	ILE	
273	260	THR	THR		THR	TYR	TYR	TYR	LEU			ARG		---	LYS	LYS	LYS	LYS		GLN	GLN	
274	261	CYS	CYS		CYS	CYS	CYS	CYS	CYS			LEU		---	VAL	VAL	VAL	VAL		LEU	LEU	
275	262	THR	THR		THR	PHE	PHE	PHE	PHE			ILE		---	THR	THR	THR	THR		TYR	TYR	
276	263	LEU	LEU		LEU	ILE	ILE	ILE	ILE			CYS		---	CYS	CYS	CYS	CYS		CYS	CYS	
277	264	ASN	ASP		ASP	TYR	TYR	TYR	TYR			GLU		---	VAL	VAL	VAL	VAL		PHE	PHE	
278	265	GLY	GLY		GLY	GLY	GLY	GLY	GLY			ALA		---	VAL	VAL	VAL	VAL		VAL	VAL	
279	266	LEU	LEU		LEU	HIS	HIS	HIS	HIS			THR		---	VAL	VAL	VAL	VAL		TYR	TYR	
280	267	ARG	ARG		ARG	ILE	ILE	ILE	ILE			ASN		---	ASP	ASP	ASP	ASP		GLY	GLY	
281	268	ASN	ASN		ASN	---	---	---	---			PHE		---	VAL	ILE	ILE	VAL		HIS	HIS	
282	269	PRO	PRO		PRO	---	---	---	---			SER		---	SER	SER	SER	SER		ILE	ILE	
283	270	GLU	GLU		GLU	---	---	---	---			PRO		---	GLU	GLN	GLN	GLU		---	---	
284	271	GLY	GLY		GLY	LEU	LEU	LEU	LEU			LYS		---	GLU	ASN	ASP	GLU		---	---	
285	272	ALA	ALA		ALA	ASN	ASN	ASN	ASN			GLN		---	GLU	ASP	ASP	GLU		---	---	
286	273	ALA	VAL		VAL	ASP	ASP	ASP	ASP			ILE		---	PRO	PRO	PRO	PRO		GLN	GLN	
287	274	---	---		---	VAL	VAL	VAL	VAL			THR		---	ASP	GLU	GLU	ASP		ASN	ASN	
288	275	PHE	PHE		PHE	SER	SER	SER	SER			VAL		---	VAL	VAL	VAL	VAL		ASP	ASP	
289	276	THR	THR		THR	VAL	VAL	VAL	VAL			---		---	GLN	ARG	HIS	GLN		VAL	VAL	
290	277	TRP	TRP		TRP	SER	SER	SER	SER			---		---	PHE	PHE	PHE	PHE		SER	SER	
291	278	GLU	GLU		GLU	TRP	TRP	TRP	TRP			SER		---	SER	SER	SER	SER		ILE	ILE	
292	279	PRO	PRO		PRO	LEU	LEU	LEU	LEU			TRP		---	TRP	TRP	TRP	TRP		HIS	HIS	
293	274	---	---		---	---	---	---	---			LEU		---	PHE	PHE	PHE	PHE		TRP	TRP	
294	275	---	---		---	---	---	---	---			GLN		---	VAL	ILE	VAL	VAL		LEU	LEU	
295	276	SER	SER		SER	MET	MET	MET	MET			ASP		---	---	---	---	---		---	---	
296	277	THR	THR		THR	ASP	ASP	ASP	ASP			GLY		---	---	---	---	---		---	---	
297	278	---	---		---	ASP	ASP	ASP	ASP			LYS		---	ASP	ASP	ASP	ASN		MET	MET	
298	279	---	---		---	---	---	---	---			PRO		---	ASN	ASP	ASP	ASN		ASP	ASP	
299	282 280	GLY	GLY		GLY	ARG	ARG	ARG	ARG			VAL		---	---	---	---	---		ASP	ASP	
300	283 281	LYS	LYS		LYS	GLU	GLU	GLU	GLU			SER		---	VAL	VAL	VAL	VAL		---	---	
301	284 282	ASP	ASP		ASP	ILE	ILE	ILE	ILE			GLY		---	ARG	GLU	GLU	GLU		ARG	ARG	
302	285 283	ALA	ALA		ALA	THR	THR	THR	THR			PHE		---	VAL	VAL	VAL	VAL		LYS	LYS	
303	286	VAL	VAL		VAL	---	---	---	---			THR		---	PHE	HIS	HIS	HIS		ILE	ILE	
304	287 284	GLN	GLN		GLN	ASP	ASP	ASP	ASP			---		---	THR	THR	THR	THR		TYR	TYR	
305	288 285	LYS	LYS		LYS	THR	THR	THR	THR			THR		---	ALA	ALA	ALA	ALA		---	---	
306	289 286	LYS	LYS		LYS	LEU	LEU	LEU	LEU			GLU		---	GLN	GLN	GLN	GLN		GLU	GLU	
307	290 287	ALA	ALA		ALA	ALA	ALA	ALA	ALA			PRO		---	THR	THR	THR	THR		THR	THR	
308	291 288	ALA	VAL		VAL	GLN	GLN	GLN	GLN			VAL		---	GLN	THR	THR	THR		HIS	HIS	
309	292 289	GLN	GLN		GLN	THR	THR	THR	THR			THR		---	PRO	HIS	ARG	GLN		ALA	ALA	
310	293 290	ASN	ASN		ASN	VAL	VAL	VAL	VAL			VAL		---	HIS	PRO	PRO	PRO		GLN	GLN	
311	294 291	SER	SER		SER	LEU	LEU	LEU	LEU			GLU		---	GLU	GLU	GLU	ARG		ASN	ASN	
312	295 292	CYS	CYS		CYS	LEU	ILE	ILE	ILE			ALA		---	GLU	GLU	GLU	GLU		VAL	VAL	
313	296 293	GLY	GLY		GLY	LYS	LYS	LYS	LYS			LYS		---	GLN	GLN	GLU	GLU		LEU	LEU	
314	297 294	CYS	CYS		CYS	GLU	GLU	GLU	GLU			GLY		---	LEU	SER	GLN	GLN		ILE	ILE	
315	295	---	---		---	GLU	GLU	GLU	GLU			---		---	---	---	PHE	TYR		LYS	LYS	
316	296	---	---		---	GLY	GLY	GLY	GLY			---		---	---	---	---	---		---	---	
317	298 297	---	---		---	LYS	LYS	LYS	LYS			SER		---	ASN	ASN	ASN	ASN		GLU	GLU	
318	299 298	---	---		---	LEU	LEU	LEU	LEU			ARG		---	---	---	---	---		GLU	GLU	
319	300 299	TYR	TYR		TYR	ALA	ALA	ALA	ALA			PRO		---	---	---	---	---		GLY	GLY	
320	301 300	SER	SER		SER	SER	SER	SER	SER			GLN		---	GLY	SER	SER	SER		LYS	LYS	
321	302 301	VAL	VAL		VAL	THR	THR	THR	THR			THR		---	THR	THR	THR	THR		LEU	LEU	
322	303 302	SER	SER		SER	CYS	CYS	CYS	CYS			TYR		---	PHE	LEU	PHE	PHE		ALA	ALA	
323	304 303	SER	SER		SER	SER	SER	SER	SER			LYS		---	ARG	ARG	ARG	ARG		SER	SER	
324	305 304	VAL	VAL		VAL	LYS	LYS	LYS	LYS			VAL		---	VAL	SER	SER	VAL		THR	THR	
325	306 305	LEU	LEU		LEU	LEU	LEU	LEU	LEU			ILE		---	VAL	VAL	VAL	VAL		TYR	TYR	
326	307 306	PRO	PRO		PRO	ASN	ASN	ASN	ASN			SER		---	SER	SER	SER	SER		SER	SER	
327	308 307	GLY	GLY		GLY	ILE	ILE	ILE	ILE			THR		---	THR	GLU	GLU	ALA		ARG	ARG	ASN
328	309 308	CYS	CYS		CYS	THR	THR	THR	THR			LEU		---	LEU	LEU	LEU	LEU		LEU	LEU	LEU
329	310 309	ALA	ALA		ALA	GLU	GLU	GLU	GLU			THR		---	HIS	PRO	PRO	PRO		ASN	ASN	ASN
330	311 310	GLU	GLU		GLU	GLN	GLN	GLN	GLN			ILE		---	ILE	ILE	ILE	ILE		ILE	ILE	ILE
331	312 311	ARG	ARG		ARG	GLN	GLN	GLN	GLN			THR		---	GLN	VAL	LEU	GLN		THR	THR	THR
332	313 312	TRP	TRP		TRP	TRP	TRP	TRP	TRP			GLU		---	HIS	HIS	HIS	HIS		GLN	GLN	GLN
333	314 313	ASN	ASN		ASN	MET	MET	MET	MET			SER		---	GLN	ARG	GLN	GLN		GLN	GLN	GLN
334	315 314	SER	SER		SER	SER	SER	SER	SER			ASP		---	ASP	ASP	ASP	ASP		GLN	GLN	GLN
335	316 315	GLY	GLY		GLY	GLY	GLU	GLU	GLU			TRP		---	TRP	TRP	TRP	TRP		GLN	GLN	GLN
336	317 316	ALA	ALA		ALA	SER	SER	SER	SER			LEU		---	MET	LEU	LEU	MET		TRP	TRP	TRP
337	318 317	SER	SER		SER	THR	THR	THR	THR			---		---	---	---	---	---		MET	MET	MET
338	319 318	PHE	PHE		PHE	PHE	PHE	PHE	PHE			---		---	---	---	---	---		---	---	
339	320 319	LYS	LYS		LYS	THR	THR	THR	THR			---		---	---	---	---	---		---	---	
340	321 320	CYS	CYS		CYS	CYS	CYS	CYS	CYS			ASN		---	SER	ASN	ASN	SER		SER	SER	SER
341	322 321	THR	THR		THR	ARG	LYS	LYS	LYS			LEU		---	GLY	GLY	GLY	GLY		GLU	GLU	GLU
342	323 322	VAL	VAL		VAL	VAL	VAL	VAL	VAL			ASN		---	LYS	LYS	ARG	LYS		SER	SER	SER
343	324 323	THR	THR		THR	THR	THR	THR	THR			VAL		---	GLU	THR	THR	GLU		THR	THR	THR
344	325 324	HIS	HIS		HIS	SER	SER	SER	SER			PHE		---	PHE	PHE	PHE	PHE		PHE	PHE	PHE
345	326 325	PRO	PRO		PRO	GLN	GLN	GLN	GLN			THR		---	LYS	LYS	ARG	LYS		THR	THR	THR
346	327 326	GLU	GLU		GLU	GLY	GLY	GLY	GLY			CYS		---	CYS	CYS	CYS	CYS		CYS	CYS	CYS
347	328 327	SER	SER		SER	VAL	VAL	VAL	VAL			ARG		---	LYS	LYS	LYS	LYS		LYS	LYS	LYS
348	329 328	GLY	GLY		GLY	ASP	ASP	ASP	ASP			VAL		---	VAL	VAL	VAL	VAL		VAL	VAL	VAL
349	330 329	THR	THR		THR	TYR	TYR	TYR	TYR			ASP		---	ASN	ASN	THR	ASN		THR	THR	THR
350	331 330	---	---		---	LEU	LEU	LEU	LEU			HIS		---	ASN	SER	SER	ASN		SER	SER	SER
351	332 331	LEU	LEU		LEU	---	---	---	---			ARG		---	LYS	GLY	ALA	LYS		GLN	GLN	GLN
351A		---	---		---	---	---	---	---			GLY		---	ASP	ALA	ALA	ALA		GLY	GLY	GLY
352	333 332	THR	THR		THR	ALA	ALA	ALA	ALA			LEU		---	LEU	PHE	PHE	LEU		GLU	GLU	GLU
353	334 333	GLY	GLY		GLY	HIS	HIS	HIS	HIS			THR		---	PRO	PRO	PRO	PRO	THR	ASN	ASN	ASN
354	335 334	THR	THR		THR	THR	THR	THR	THR			CYS		---	SER	ALA	SER	SER	PRO	TYR	TYR	TYR
355	336 335	ILE	ILE		ILE	ARG	ARG	ARG	ARG			LEU		---	PRO	PRO	PRO	PRO	---	TRP	TRP	TRP
356	336	---	---		---	ARG	ARG	ARG	ARG			LYS		---	ILE	ILE	ILE	ILE	LEU	---	---	---
357	337 337	ALA	ALA		ALA	CYS	CYS	CYS	CYS			ASN		---	GLU	GLU	GLU	GLU	THR	ALA	ALA	ALA
358	338 338	LYS	LYS		LYS	PRO	PRO	PRO	PRO			VAL		---	LYS	LYS	LYS	LYS	GLY	HIS	HIS	HIS
359	339 339	VAL	SER		VAL	---	---	---	---			SER		---	THR	SER	THR	THR	LYS	THR	THR	THR
360	340	THR	GLN		THR	---	---	---	---			SER		---	ILE	ILE	ILE	ILE	ILE	ARG	ARG	ARG
												THR		---	---	---	---	---	---	---	---	---
												CYS		---	SER	SER	SER	SER	ALA	CYS	CYS	CYS
												ALA		---	LYS	LYS	LYS	LYS	LYS	SER	SER	SER
												ALA		---	PRO	PRO	PRO	PRO				

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

	EU INDEX	OU INDEX	121 PMJ 'CL	122 PMES 'CL	123 RABBIT IGG	124 PGAMMA B1-12, 14'CL	125 RAB IGG #	126 RAB IGG 'CL	127 P2A2 'CL #	128 39-1A, 20B 'CL	129 PA19 'CL	130 CT-12	131 PIKA	132 HA-3	133 HA-11	134 HA-1	135 HA-5	136 HA-27	137 SYRIAN HAMSTER IGM 'CL	138 GP IGG	139 GP IGG
243A			---	---	---	---	---		---	---	---								---	---	
243B			---	---	---	---	---		---	---	---								---	---	
243C			---	---	---	---	---		---	---	---								---	---	
243D			---	---	---	---	---		---	---	---								---	---	
243E			---	---	---	---	---		---	---	---								---	---	
243F			---	---	---	---	---		---	---	---								---	---	
243G		230	VAL	---	---	---	---		---	---	---								VAL	---	
243H		231	ASP	---	---	---	---		---	---	---								VAL	---	
243I		232	SER	---	---	---	---		---	---	---								THR	---	
244	231		---	---	PRO	PRO	PRO		PRO	PRO	ILE								---	ALA	
245	232		---	---	PRO	PRO	PRO		PRO	PRO	SER								---	PRO	
245A			---	---	---	---	---		---	---	---								---	---	
245B			---	---	---	---	---		---	---	---								---	---	
245C			---	---	---	---	---		---	---	---								---	---	
246	233	233	GLU	---	GLU	GLU	GLU		GLU	GLU	---								GLU	GLX	
247	234	234	LEU	---	LEU	LEU	LEU		LEU	LEU	GLY								MET	LEU	
248	235	235	PRO	---	LEU	LEU	LEU		LEU	LEU	CYS								ASN	LEU	
249	236	236	PRO	---	GLY	GLY	GLY		GLY	GLY	GLN								PRO	GLY	
250	237	237	ASN	---	GLY	GLY	GLY		GLY	GLY	---								ASN	GLY	
251	238	238	VAL	---	PRO	PRO	PRO		PRO	PRO	PRO								VAL	PRO	
251A			---	---	---	---	---		---	---	---								---	---	
251B			---	---	---	---	---		---	---	---								---	---	
252	239	239	SER	---	SER	SER	SER		SER	SER	SER								SER	SER	
253	240	240	VAL	---	VAL	VAL	VAL		VAL	VAL	LEU								VAL	VAL	
254	241	241	PHE	---	PHE	PHE	PHE		PHE	PHE	SER								PHE	PHE	
255	242	242	---	---	ILE	ILE	ILE		ILE	ILE	LEU								VAL	ILE	
256	243		ILE	---	PHE	PHE	PHE		PHE	PHE	GLN								---	PHE	
257	244	243	PRO	---	PRO	PRO	PRO		PRO	PRO	ARG								PRO	PRO	
258	245	244	PRO	---	PRO	PRO	PRO		PRO	PRO	PRO								SER	PRO	
259	246	245	ARG	---	LYS	LYS	LYS		LYS	LYS	ASP								ARG	LYS	
260	247	246	ASP	---	PRO	PRO	PRO		PRO	PRO	LEU								ASP	PRO	
261	248	247	SER	---	LYS	LYS	LYS		LYS	LYS	GLY								ALA	LYS	
262	249	248	PHE	---	ASP	ASP	ASP		ASP	ASP	ASP								PHE	ASX	
263	250		SER	---	THR	THR	THR		THR	THR	---								SER	THR	
264	251	249	GLY	---	LEU	LEU	LEU		LEU	LEU	LEU								GLY	LEU	
265	252	250	SER	---	MET	MET	MET		MET	MET	LEU								PRO	MET	
266	253	251	GLY	---		ILE	ILE		ILE	ILE	LEU	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ALA	ILE	
267	254	252	THR	---		SER	SER		SER	SER	GLY	SER	SER	SER	SER	SER	SER	SER	PRO	SER	
268	255	253	ARG	---		ARG	ARG		ARG	ARG	ARG	VAL	LEU	LEU	LEU	LEU	LEU	LEU	ARG	LEU	
269	256	254	LYS	---		THR	THR		THR	THR	ASP	THR	THR	THR	THR	THR	THR	THR	LYS	THR	
270	257	255	SER	---		PRO	PRO		PRO	PRO	ALA	PRO	PRO	PRO	PRO	PRO	PRO	PRO	SER	PRO	
271	258	256	ARG	---		GLU	GLU		GLU	GLU	SER	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ARG	LYS	
272	259	257	LEU	---		VAL	VAL		VAL	VAL	LEU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	LEU	ALA	
273	260	258	ILE	---		THR	THR		THR	THR	THR	THR	SER	THR	THR	THR	THR	THR	PHE	THR	
274	261	259	CYS	---		CYS	CYS		CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	
275	262	260	GLN	---		VAL	VAL		VAL	VAL	THR	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLU	VAL	
276	263	261	ALA	---		VAL	VAL		VAL	VAL	LEU	VAL	VAL	VAL		VAL		VAL	ALA	VAL	
277	264	262	THR	---		VAL	VAL		VAL	VAL	SER	VAL	VAL	VAL		VAL		VAL	SER	VAL	
278	265	263	GLY	---		ASP	ASP		ASP	ASP	GLY	ASP	ASP	ASP		ASP		ASP	ASN	ASP	
279	266	264	PHE	---		VAL	VAL		VAL	VAL	LEU	VAL	VAL	VAL		VAL		VAL	PHE	VAL	
280	267	265	SER	---		SER	SER		SER	SER	LYS	SER	SER	SER		SER		SER	SER	SER	
281	268	266	PRO	---		GLN	GLU	GLU	GLU	GLU	ASN	GLN	GLU	GLU		GLN		GLU	PRO	GLN	
282	269	267	LYS	---		ASP	ASP	ASP	ASP	ASP	PRO	ASP	ASP	ASP		ASP		ASP	LYS	GLU	
283	270	268	GLN	---		ASP	ASP	ASP	ASP	ASP	GLU	ASP	ASP	ASP		ASP		ASP	GLN	ASP	
284	271		ILE	---		PRO	PRO	PRO	PRO	PRO	ASP	PRO	PRO	PRO		PRO		PRO	ILE	LEU	
285	272		SER	---		GLU	GLU	GLU	GLU	GLU	ALA	GLU	GLU	GLU		GLU		GLU	THR	GLU	
286	273	269	VAL	---		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL		VAL		VAL	VAL	VAL	
287	274		---	---		GLN	GLX	GLN	GLN	GLN	---	GLN	GLN	GLN		GLN		GLN	---	GLN	
288	275		---	---		PHE	PHE	PHE	PHE	PHE	PHE	VAL	PHE	PHE		PHE		PHE	---	PHE	
289	276	270	SER	---		THR	THR	THR	THR	THR	THR	THR	THR	THR		THR			SER	THR	
290	277	271	TRP	---		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP		TRP			TRP	TRP	
291	278	272	LEU	---		TYR	TYR	TYR	TYR	TYR	GLU	TYR	TYR	TYR		TYR			LEU	TYR	
292	279	273	ARG	---		ILE	ILE	ILE	ILE	ILE	PRO	ILE	ILE	ILE		ILE			ARG	MET	
293		274	ASP	---		---	---	---	---	---	---	---	---	---		---			ASP	---	
294		275	GLY	---		---	---	---	---	---	---	---	---	---		---			GLY	---	
295	280	276	GLN	---		ASN	ASX	ASN	ASN	ASN	THR	ASP	ASP	ASP		ASP			LYS	GLY	
296	281	277	LYS	---		ASN	ASX	ASN	ASN	ASN	ASN	ASN	ASN	ASN		ASN			PRO	ASN	
297		278	VAL	---		---	---	---	---	---	---	---	---	---		---			VAL	---	
298		279	GLU	---		---	---	---	---	---	---	---	---	---		---			LYS	---	
299	282	280	SER	---		GLU	GLX	GLU	GLU	GLU	GLY	GLU	GLU	GLU		LYS			SER	LYS	
300	283	281	GLY	---		GLN	GLN	GLN	GLN	GLN	ASN		GLN	GLU		GLN			GLY	LEU	
301	284	282	VAL	---		VAL	VAL	VAL	VAL	VAL	GLU		VAL	VAL		VAL			PHE	MET	
302	285	283	LEU	---		ARG	ARG	ARG	ARG	ARG	PRO		ARG	ARG		ARG			THR	ASX	
303	286		---	---		THR	THR	THR	THR	THR	VAL			THR		THR			---	THR	
304	287	284	THR	---		ALA	ALA	ALA	ALA	ALA	GLN			ALA		ALA			THR	ALA	
305	288	285	LYS	---		ARG	ARG	ARG	ARG	ARG	GLN			ARG		ARG			GLU	GLX	
306	289	286	PRO	---		PRO	PRO	PRO	PRO	PRO	ARG			PRO		PRO			PRO	ALA	
307	290	287	VAL	---		PRO	PRO	PRO	PRO	PRO	ALA			PRO		PRO			VAL	ASX	
308	291	288	GLU	---		LEU	LEU	LEU	LEU	LEU	GLN			LEU		LEU			THR	VAL	
309	292	289	ALA	---		ARG	ARG	ARG	ARG	ARG	ARG			ARG		ARG			PRO	LEU	
310	293	290	GLU	---		GLU	GLU	GLU	GLU	GLU	ASP		GLU	GLU		GLU			GLU	GLX	
311	294	291	THR	---		GLN	GLN	GLN	GLN	GLN	LEU		GLN	GLN		GLN			ASP	GLX	
312	295	292	LYS	---		GLN	GLN	GLN	GLN	GLN	SER		GLN	GLN		GLN			ARG	GLX	
313	296	293	GLY	---		PHE	PHE	PHE	PHE	PHE	GLY		PHE	PHE		PHE			GLY	PHE	
314	297	294	ALA	---		ASN	ASP	ASN	ASN	ASN	CYS		ASP	ASP					SER	ASN	
315		295	GLY	---		---	---	---	---	---	---		---	---					GLY	---	
316		296	PRO	---		---	---	---	---	---	---		---	---					PRO	---	
317	298	297	ALA	---		SER	SER	SER	SER	SER	---		SER	SER					ARG	GLY	
318	299	298	THR	---		THR	THR	THR	THR	THR	---		THR	THR					THR	THR	
319	300	299	PHE	---		ILE	ILE	ILE	ILE	ILE	TYR		LEU	ILE					TYR	PHE	
320	301	300	SER	---		ARG	ARG	ARG	ARG	ARG	SER			ARG					LYS	ARG	
321	302	301	ILE	---		VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	
322	303	302	SER	---		VAL	VAL	VAL	VAL	VAL	SER	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ILE	VAL	
323	304	303	SER	---		SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	
324	305	304	MET	---		THR	THR	THR	THR	THR	VAL	THR	THR	THR	THR	ILE	ILE	THR	THR	ALA	
325	306	305	LEU	---		LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
326	307	306	THR	---		PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	THR	THR	
327	308	307	ILE	---		ILE	ILE	ILE	ILE	ILE	SER	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	
328	309	308	THR	---		THR	ALA	ALA	ALA	ALA	SER	ALA	ALA	ALA	ALA	ALA	ALA	LYS	THR	GLX	
329	310	309	GLU	---		HIS	HIS	HIS	HIS	HIS	ALA	HIS	HIS	HIS	HIS	HIS	HIS	HIS	GLU	HIS	
330	311	310	SER	---		GLN	GLU	GLN	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	SER	ASX	
331	312	311	ASP	---		ASP	ASP	ASP	ASP	ASP	THR	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP		
332	313	312	TRP	---		TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	
333	314	313	LEU	---		LEU	LEU	LEU	LEU	LEU	LYS	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
334	315	314	SER	---		ARG	ARG	ARG	ARG	ARG	ALA	ARG	LYS	ARG	ARG	SER	SER	ARG	ASN		
335	316	315	GLN	---		GLY	GLY	GLY	GLY	GLY	ARG	GLY	GLY	GLY	GLY	GLY	GLY	GLY	LEU		
336	317	316	SER	---		LYS	LYS	LYS	LYS	LYS	THR	LYS	LYS	LYS	LYS	LYS	LYS	LYS	SER		
337	318	317	LEU	---		GLU	GLU	GLU	GLU	GLU	GLU			GLU		GLU			VAL		
338	319	318	TYR	---		PHE	PHE	PHE	PHE	PHE	PHE			PHE		PHE			TYR		
339	320	319	THR	---		LYS	LYS	LYS	LYS	LYS	THR			LYS		LYS			THR		
340	321	320	CYS	---		CYS	CYS	CYS	CYS	CYS	CYS			CYS		CYS			CYS		
341	322	321	ARG	---		LYS	LYS	LYS	LYS	LYS	THR			LYS		LYS			ARG		
342	323	322	VAL	---		VAL	VAL	VAL	VAL	VAL	VAL			VAL		VAL			VAL		
343	324	323	ASP	---		HIS	HIS	HIS	HIS	HIS	THR			HIS		HIS			ASP		
344	325	324	HIS	---		ASN	ASP	ASN	ASN	ASN	HIS			ASP		ASP			HIS		
345	326	325	ARG	---		LYS	LYS	LYS	LYS	LYS	PRO			LYS		LYS			ARG		
346	327	326	GLY	---		ALA	ALA	ALA	ALA	ALA	GLU		ALA	ALA		ALA			GLY		
347	328	327	ILE	---		LEU	LEU	LEU	LEU	LEU	ILE		LEU	LEU		LEU			LEU		
348	329	328	PHE	---		PRO	PRO	PRO	PRO	PRO	ASP		PRO	PRO					THR		
349	330	329	PHE	---		ALA	ALA	ALA	ALA	ALA	SER		ALA	SER					PHE		
350	331	330	ASP	---		PRO	PRO	PRO	PRO	PRO	GLY			PRO					TRP		
351	332	331	LYS	---		ILE	ILE	ILE	ILE	ILE	SER			ILE					LYS	ILE	ILE
351A			ASN	---		---	---	---	---	---	LEU			---					---	---	---
352	333	332	VAL	---		GLU	GLU	GLU	GLU	GLU	THR			GLU					ASN	THR	THR
353	334	333	SER	---		LYS	LYS	LYS	LYS	LYS	ALA			LYS					VAL	ARG	ARG
354	335	334	MET	---		THR	THR	THR	THR	THR	THR			THR					SER	THR	THR
355	336	335	SER	---		ILE	ILE	ILE	ILE	ILE	ILE			ILE					SER	ILE	ILE
356		336	SER	---		---	---	---	---	---	SER			---					THR	---	---
357	337	337	GLU	---		SER	SER	SER	SER	SER	ARG			SER					CYS	SER	SER
358	338	338	CYS	---		LYS	LYS	LYS	LYS	LYS	GLY			LYS					ALA	LYS	LYS
359	339	339	SER	---		ALA	ALA	ALA	ALA	ALA	---			ALA					ALA	ALA	ALA
360	340		THR	---		ARG	ARG	ARG	ARG	ARG	---			LYS					---	LYS	LYS

HEAVY CONSTANT CHAINS CH2 REGION (cont'd)

EU INDEX	OU INDEX	140 GP IGG2	141 MOO	142 PIG IGG	143 SHEEP pSHC 'CL #	144 HORSE IGG #	145 BOVINE IGG	146 GOAT IGG	147 CHICKEN IGM 'CL #	148 Elops VH 'CL #	149 Re4b 'CL	150 Re20 'CL	151 Xenopus laevis IgY 'CL	152 Xenopus laevis c8(II) 'CL #	153 Xenopus laevis c14(II) 'CL #	154 Xenopus laevis c35 'CL	155 Xenopus laevis c40(II) 'CL
243A		---	---		---				---	---	---	---	---	---			
243B		---	---		---				---	---	---	---	---	---			
243C		---	---		---				---	---	---	---	---	---			
243D		---	---		---				---	---	---	---	---	---			
243E		---	---		---				---	---	---	---	---	---			
243F		---	---		---				---	---	---	---	---	---			
243G	230	---	VAL		---				ILE	GLU	ASP	---	CYS	PRO			
243H	231	---	MET		---				PRO	PRO	ARG	---	GLN	VAL			
243I	232	---	LEU		---				THR	PRO	VAL	---	ASP	LYS			
244 231		PRO	---		PRO				---	---	---	---	GLU	PRO			
245 232		PRO	---		PRO				---	---	---	---	---	---			
245A		---	---		---				---	---	---	---	---	---			
245B		---	---		---				---	---	---	---	---	---			
245C		---	---		---				---	---	---	---	---	---			
246 233	233	GLU	THR		GLU				PRO	LYS	VAL	---	PRO	VAL			
247 234	234	ASN	LEU		LEU				ASN	PRO	HIS	---	GLU	GLU			
248 235	235	LEU	PRO		PRO				GLY	PRO	HIS	PRO	PRO	LYS			
249 236	236	GLY	PRO		GLY				ILE	ARG	PRO	GLN	ILE	PRO			
250 237	237	GLY	GLU		GLY				PRO	GLN	THR	ALA	GLU	VAL			
251 238	238	PRO	VAL		PRO				LEU	PRO	VAL	PRO	PRO	VAL			
251A		---	---		---				---	---	---	---	---	---			
251B		---	---		---				---	---	---	---	---	---			
252 239	239	SER	SER		SER				PHE	VAL	THR	GLN	THR	SER			
253 240	240	VAL	GLY		VAL				VAL	LEU	ILE	LEU	VAL	ILE			
254 241	241	PHE	PHE		PHE				THR	SER	THR	ILE	GLU	HIS			
255 242	242	ILE	ILE		ILE				MET	ILE	ILE	PRO	ILE	PRO			
256 243		PHE	---		PHE				HIS	---	---	---	---	---			
257 244	243	PRO	PRO		PRO				PRO	MET	---	LEU	LEU	PRO			
258 245	244	PRO	PRO		PRO				PRO	THR	---	VAL	GLN	SER			
259 246	245	LYS	ARG		LYS				SER	PRO	THR	PRO	GLY	LYS			
260 247	246	PRO	ASP		PRO				ARG	SER	ALA	SER	PRO	ASP			
261 248	247	LYS	ALA		LYS				GLU	GLN	LEU	PRO	CYS	ALA			
262 249	248	ASP	PHE		ASP				ASP	GLU	ASP	GLU	ALA	LEU			
263 250		THR	---		THR				PHE	GLU	GLU	THR	SER	ALA			
264 251	249	LEU	PHE		LEU				GLU	LEU	ILE	LEU	SER	LEU			
265 252	250	MET	GLY		THR				GLY	THR	LYS	HIS	LYS	ASN			
266 253	251	ILE	ASX		ILE				PRO	LEU	ARG	ASN	SER	GLU			
267 254	252	SER	PRO		SER				PHE	ASN	GLN	GLN	VAL	SER			
268 255	253	LEU	ARG		GLY				ARG	LYS	GLY	THR	GLU	LEU			
269 256	254	THR	LYS		THR				ASN	THR	LYS	THR	LEU	PHE			
270 257	255	PRO	GLU		PRO				ALA	ALA	ALA	ALA	---	---			
271 258	256	ARG	PRO		GLU				SER	THR	ILE	VAL	---	---			
272 259	257	VAL	LEU		VAL				ILE	PHE	ALA	LEU	---	ILE			
273 260	258	THR	ILE		THR				LEU	ALA	VAL	GLY	LEU	VAL			
274 261	259	CYS	CYS		CYS				CYS	CYS	CYS	CYS	CYS	CYS			
275 262	260	VAL	GLN		VAL				GLN	LEU	LEU	MET	LEU	LEU			
276 263	261	VAL	ALA		VAL				THR	ALA	VAL	ILE	ILE	ALA			
277 264	262	VAL	SER		VAL				ARG	THR	ASN	SER	THR	THR			
278 265	263	ASP	GLY		ASP				GLY	ASP	ASP	GLY	GLY	ASN			
279 266	264	VAL	PHE		VAL				ARG	PHE	PHE	PHE	TYR	PHE			
280 267	265	SER	SER		GLY				ARG	TYR	THR	SER	ALA	THR			
281 268	266	GLN	PRO		GLN				ARG	PRO	PRO	PRO	PRO	PRO			
282 269	267	ASP	ARG		ASP				---	LYS	ALA	ASP	SER	THR			
283 270	268	GLU	GLN		ASP				PRO	GLY	ILE	ASN	GLU	HIS			
284 271		PRO	---		PRO				THR	HIS	PHE	ILE	ILE	ILE			
285 272		GLU	---		GLU				GLU	SER	THR	LYS	LYS	VAL			
286 273	269	VAL	VAL		VAL				VAL	PHE	VAL	VAL	VAL	ILE			
287 274		GLN	---		GLN				---	---	---	---	---	---			
288 275		PHE	---		PHE				---	---	---	---	---	---			
289 276	270	THR	TRP		SER				THR	LYS	ASN	SER	HIS	LYS			
290 277	271	TRP	SER		TRP				TRP	TRP	TRP	TRP	TRP	TRP			
291 278	272	PHE	LEU		PHE				TYR	LEU	LEU	LYS	LEU	LEU			
292 279	273	VAL	ARG		VAL				LYS	ARG	LYS	LYS	LEU	LYS			
293	274	---	ASP		---				ASN	ASP	ASN	ALA	ASN	ASN			
294	275	---	GLY		---				GLY	GLY	GLY	GLY	GLY	GLY			
295 280	276	ASP	LYS		ASP				SER	LYS	LYS	LEU	GLN	ASN			
296 281	277	ASN	GLN		ASN				PRO	GLU	PRO	ASN	VAL	GLN			
297	278	---	ILE		---				VAL	VAL	LEU	GLN	THR	THR			
298	279	---	GLU		---				---	THR	ASP	ALA	ASN	THR			
299 282	280	LYS	SER		VAL				---	ASP	SER	GLY	ILE	GLU			
300 283	281	PRO	GLY		GLU				---	GLY	GLY	VAL	SER	GLY			
301 284	282	VAL	VAL		VAL				---	ILE	ILE	VAL	PRO	VAL			
302 285	283	GLY	THR		ARG				---	ALA	VAL	LEU	SER	ARG			
303 286		ASN	---		THR				---	---	---	---	---	---			
304 287	284	ALA	THR		ALA				---	---	---	---	ASN	VAL			
305 288	285	GLU	ASN		ARG				---	THR	THR	PRO	SER	GLU			
306 289	286	THR	GLU		THR				ALA	LEU	SER	SER	LYS	GLU			
307 290	287	LYS	VAL		LYS				ALA	THR	PRO	THR	PRO	PRO			
308 291	288	PRO	GLX		PRO				ALA	GLU	ALA	PRO	CYS	VAL			
309 292	289	ARG	ALA		ARG				ALA	CYS	PHE	ARG	LYS	GLU			
310 293	290	VAL	GLX		GLU				THR	GLN	GLN	THR	GLU	ASP			
311 294	291	GLU	ALA		GLU				THR	LYS	VAL	ASN	GLU	LYS			
312 295	292	GLN	LYS		GLN				ALA	LYS	ASN	GLY	ASN	LYS			
313 296	293	TYR	GLX		PHE				THR	GLY	GLY	GLY	GLY	ARG			
314 297	294	ASN	SER		ASN				---	---	---	---	---	---			
315	295	---	GLY		---				THR	---	---	---	THR	GLY			
316	296	---	PRO		---				VAL	ASP	THR	---	PHE	TYR			
317 298	297	THR	THR		SER				GLY	LYS	GLY	---	SER	GLU			
318 299	298	THR	THR		THR				PRO	SER	ASN	---	SER	ALA			
319 300	299	PHE	TYR		PHE				GLU	PHE	PHE	PHE	ARG	THR			
320 301	300	ARG	LYS		ARG				VAL	THR	SER	GLU	SER	SER			
321 302	301	VAL	VAL		VAL				VAL	ALA	ALA	THR	LYS	TYR			
322 303	302	GLU	THR		VAL				ALA	SER	THR	VAL	VAL	LEU			
323 304	303	SER	SER		SER				GLU	SER	SER	ALA	SER	SER			
324 305	304	VAL	MET		ALA				SER	PHE	GLN	TYR	VAL	ILE			
325 306	305	LEU	LEU		LEU				ARG	LEU	LEU	LEU	PRO	THR			
326 307	306	PRO	THR		PRO				ILE	GLN	THR	PRO	LYS	ARG			
327 308	307	ILE	ILE		ILE				SER	ALA	PHE	LEU	GLU	LYS			
328 309	308	GLN	GLN		GLN				VAL	SER	THR	ASN	ASP	GLU			
329 310	309	HIS	GLU		HIS				THR	GLU	ALA	VAL	TRP	TRP			
330 311	310	GLN	GLN		GLN				GLU	SER	GLU	GLU	ASN	ASP			
331 312	311	ASP	ALA		ASP				SER	GLN	GLU	GLU	SER	LEU			
332 313	312	TRP	TRP		TRP				GLU	TRP	TRP	TRP	GLU	ASP			
333 314	313	LEU	LEU		THR				TRP	LYS	PHE	THR	ASP	THR			
		---	---		---				ASP	ARG	GLY	ASN	SER	LEU			
		---	---		---				---	---	---	---	---	---			
334 315	314	ARG	SER		GLY				---	---	---	---	---	---			
335 316	315	GLY	GLN		GLY				THR	LEU	---	---	TYR	TYR			
336 317	316	LYS	SER		LYS				GLY	ASP	ASP	LYS	THR	SER			
337 318	317	GLU	VAL		GLU				ALA	GLY	PHE	GLN	CYS	CYS			
338 319	318	PHE	PHE		PHE				THR	THR	VAL	GLU	LYS	VAL			
339 320	319	LYS	THR		LYS				PHE	PHE	TYR	TYR	VAL	VAL			
340 321	320	CYS	CYS		CYS				SER	THR	THR	THR	THR	GLU			
341 322	321	LYS	LYS		LYS				CYS	CYS	CYS	CYS	HIS	HIS			
342 323	322	VAL	VAL		VAL				VAL	GLN	GLN	GLU	PRO	ALA			
343 324	323	TYR	GLU		HIS				VAL	PHE	VAL	VAL	ALA	GLU			
344 325	324	ASN	HIS		ASN				GLU	ILE	ASN	THR	SER	SER			
345 326	325	LYS	ARG		GLU				GLY	GLN	HIS	HIS	HIS	GLY			
346 327	326	ALA	GLY		ALA				GLU	GLU	GLU	ALA	THR	SER			
347 328	327	LEU	LEU		LEU				MET	GLY	LYS	PRO	LYS	LEU			
348 329	328	PRO	THR		PRO				ARG	GLU	ASP	SER	THR	GLN			
349 330	329	ALA	PHE		ALA				ASN	ILE	LEU	GLY	GLU	GLU			
350 331	330	PRO	GLN		PRO				THR	THR	LYS	PHE	ALA	LYS			
351 332	331	ILE	GLN		ILE				SER	GLU	SER	SER	---	ASN			
351A		---	---		---				LYS	GLN	---	---	---	MET			
352 333	332	GLU	ASN		VAL				---	THR	---	---	---	---			
353 334	333	LYS	ALA		ARG				ARG	VAL	GLN	ASP	SER	SER			
354 335	334	THR	SER		THR				MET	LYS	ASN	LYS	THR	LYS			
355 336	335	ILE	SER		ILE				GLU	TYR	ILE	ILE	---	SER			
356	336	---	MET		---				CYS	SER	SER	ASN	LYS	LEU			
357 337	337	SER	CYS		SER				GLY	SER	MET	MET	LYS	MET			
358 338	338	LYS	THR		ARG				LEU	ALA	PRO	ARG	CYS	CYS			
359 339	339	THR	SER		THR				GLU	GLU	PRO	TYR	ASP	ASP			
360 340		LYS	---		LYS				PRO	CYS	---	---	GLU	THR			
									---	SER	---	---	---	---			

HEAVY CONSTANT CHAINS CH2 REGION (Cont'd)

EU INDEX	OU INDEX	156 Xenopus laevis J2(I) 'CL	157 Xenopus laevis J4(III) 'CL	158 Xenopus laevis J6(I) 'CL	159 Xenopus laevis J12(IV) 'CL	# OF SEQUENCES	# OF AMINO ACIDS	OCCURRENCES OF MOST COMMON AMINO ACID	VARIABILITY
243A						4	1	4(VAL)	
243B						4	1	4(PRO)	
243C						4	1	4(SER)	
243D						5	1	5(THR)	
243E						5	1	5(PRO)	
243F						5	1	5(PRO)	
243G		230				35	8	18(VAL)	
243H		231				36	8	8(VAL)	
243I		232				40	9	11(+)	
244	231					63	6	37(ALA)	10.
245	232					59	5	45(PRO)	6.6
245A						9	2	5(THR)	
245B						9	1	9(PRO)	
245C						12	2	9(PRO)	
246	233	233				91	10	44(GLU),41(GLU)	21.,22.
247	234	234				95	12	48(LEU)	24.
248	235	235				96	13	36(LEU)	35.
249	236	236				96	8	43(GLY)	16.
250	237	237				95	12	44(GLY)	26.
251	238	238				94	6	54(PRO)	10.
251A						12	1	12(CYS)	
251B						12	2	8(HIS)	
252	239	239				97	8	60(SER)	13.
253	240	240				97	8	73(VAL)	11.
254	241	241				96	11	62(PHE)	17.
255	242	242				94	8	36(ILE)	21.
256	243					76	6	47(PHE)	9.7
257	244	243				94	8,9	64(PRO)	12.,13.
258	245	244				93	8	65(PRO)	11.
259	246	245				94	10	41(LYS)	23.
260	247	246				94	10,11	35(PRO)	27.,30.
261	248	247				96	10,11	46(LYS)	21.,23.
262	249	248				96	8	57(ASP),56(ASP)	13.,14.
263	250					85	12	29(THR)	35.
264	251	249				96	7	66(LEU)	10.
265	252	250				97	11	41(MET)	26.
266	253	251				103	10,11	53(ILE)	19.,21.
267	254	252				101	10	47(SER)	21.
268	255	253				99	11	38(ARG)	29.
269	256	254				99	9	57(THR)	16.
270	257	255				97	5	48(PRO)	10.
271	258	256				97	11	31(GLU),29(GLU)	34.,37.
272	259	257				98	5	47(VAL)	10.
273	260	258				98	9	65(THR)	14.
274	261	259				98	1	98(CYS)	1.
275	262	260				99	7	49(VAL)	14.
276	263	261				97	5	59(VAL)	8.2
277	264	262				97	7	50(VAL)	14.
278	265	263				96	3	48(ASP)	6.
279	266	264				96	8	42(VAL)	18.
280	267	265				94	9	54(SER)	16.
281	268	266				85	9	20(+)	38.
282	269	267				84	9	27(ASP)	28.
283	270	268				85	9	47(ASP)	16.
284	271					82	9	51(PRO)	14.
285	272					93	10	34(GLU),32(GLU)	27.,29.
286	273	269				93	6	73(VAL)	7.6
287	274					70	7,8	36(GLN),34(GLN)	14.,16.
288	275					75	6	48(PHE)	9.4
289	276	270				94	8	30(SER)	25.
290	277	271				93	4	79(TRP)	4.7
291	278	272				94	8	28(TYR)	27.
292	279	273				94	9	37(VAL)	23.
293		274				22	5	10(ASP)	11.
294		275				22	2	21(GLY)	2.1
295	280	276				90	11	31(ASP),30(ASP)	32.,33.
296	281	277				94	11	27(ASN),25(ASN)	38.,41.
297		278				30	7	16(VAL)	13.
298		279				22	8	7(GLU)	25.
299	282	280				93	8,9	35(VAL)	21.,24.
300	283	281				91	10	33(GLU),32(GLU)	28.
301	284	282				91	9	57(VAL)	14.
302	285	283				91	13	30(HIS)	39.
303	286					59	5	23(THR)	13.
304	287	284				88	7	42(ALA)	15.
305	288	285				91	12	22(LYS)	50.
306	289	286				92	11	34(THR)	30.
307	290	287				92	11	19(+)	53.
308	291	288				91	11	24(PRO)	42.
309	292	289				91	15	39(ARG)	35.
310	293	290				91	8	51(GLU),46(GLU)	14.,16.
311	294	291				91	11	28(GLU),26(GLU)	36.,38.
312	295	292				91	12,13	33(GLN),31(GLN)	33.,38.
313	296	293				91	9,10	26(GLY)	31.,35.
314	297	294				87	9	40(ASN),34(ASN)	20.,23.
315		295				32	8	12(GLU)	21.
316		296				32	5	15(PRO)	11.
317	298	297				75	10	39(SER)	19.
318	299	298				76	6	56(THR)	8.1
319	300	299				91	10	36(TYR)	25.
320	301	300				90	8	39(ARG)	18.
321	302	301				96	7	73(VAL)	9.2
322	303	302				96	10	45(VAL)	21.
323	304	303				95	6	90(SER)	6.3
324	305	304				96	11	30(VAL)	35.
325	306	305				96	7	90(LEU)	7.5
326	307	306				97	10	41(+)	24.
327	308	307				97	9	52(ILE)	17.
328	309	308				97	12	15(GLN),14(GLN)	78.,83.
329	310	309				97	8	46(HIS)	17.
330	311	310				96	8	49(GLN),46(GLN)	16.,17.
331	312	311				94	11	53(ASP),51(ASP)	20.
332	313	312				95	5	90(TRP)	5.3
333	314	313				95	9	54(LEU)	16.
334	315	314				94	11	35(SER)	30.
335	316	315				96	9	63(GLY)	14.
336	317	316				98	11	51(LYS)	21.
337	318	317				93	8	42(GLU)	18.
338	319	318				93	3	56(PHE)	5.
339	320	319				92	5	46(LYS)	10.
340	321	320				92	2	90(CYS)	2.
341	322	321				92	8	48(LYS)	15.
342	323	322				92	5	77(VAL)	6.
343	324	323				93	9	20(+)	42.
344	325	324				92	7	35(ASN)	18.
345	326	325				93	9	35(LYS)	24.
346	327	326				94	9	34(GLY)	25.
347	328	327				94	12	61(LEU)	18.
348	329	328				94	10	46(PRO)	20.
349	330	329				94	8	31(ALA)	24.
350	331	330				87	9	49(PRO)	16.
351	332	331				79	7	44(ILE)	13.
351A						3	3	1(+)	
352	333	332				95	10	41(GLU)	23.
353	334	333				96	10	37(LYS)	26.
354	335	334				95	9	66(THR)	13.
355	336	335				96	7	56(ILE)	12.
356		336				34	6	10(MET)	20.
357	337	337				95	8	48(SER)	16.
358	338	338				96	12	58(LYS)	20.
359	339	339				74	8	23(ALA)	26.
360	340					61	7	34(LYS)	13.